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RESULT 1
US-10-355-975A-38
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Sequence 11, Appl
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                                                                                                     January 22, 2005, 06:30:32; Search time 16.3133 Seconds (without alignments) 1028.511 Million cell updates/sec
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1 YEFLETLGKGTYGKVKKARE......VNPTRRATLEDVASHWWVNW
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Compugen Ltd.
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US-09-579-664B-11

US-10-355-975A-11

US-08-677-298-33

US-09-523-849-33

US-09-523-849-34

US-09-538-09-4

US-09-538-09-4

US-09-538-09-1022

US-09-538-09-1022

US-09-538-09-1022

US-09-538-09-1022

US-09-633-328B-3

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1

US-09-101-146-1
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                                                                                                                                                                                                                                                                                   478139 seqs, 66318000 residues
             GenCore version (c) 1993 - 2005
                                                                                                                                                                     US-09-980-464-11_COPY_S7_309
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Maximum Match 100%
Listing first 45 summaries
                                                                        protein search, using sw model
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seq length: 200000000
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Maximum DB
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Sequence 1841, A Sequence 34, Appl Sequence 2, Appli Sequence 2, Appli Sequence 154, Appl Sequence 28, Appl Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 6, Appli
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Patent No. 675923

GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
APPLICANT: Martin, Unia
APPLICANT: Martin, Unia
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REFERENCE: 2923-B
CURRENT APPLICATION NUMBER: US/10/355,975A
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 38
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US-09-248-756A-18441

US-09-248-756A-18441

US-10-116-326-2

US-10-103-690-2

US-10-003-690-2

US-09-930-111-2

US-09-538-092-154

US-09-538-092-154

US-09-270-767-32886

US-09-734-673-2

US-09-533-692-2

US-09-248-758-2

US-09-248-758-2

US-09-248-758-2

US-09-248-758-2

US-09-248-768-18435

US-09-248-796A-18435

US-09-248-796A-18435

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US-09-930-181-17
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; Pred. No. 7.7e-130;
0; Mismatches 0;
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US-09-579-664B-11
; Sequence 11, Application US/09579664B
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Best Local Similarity 100.0
Matches 253; Conservative
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US-10-355-975A-38
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117 IAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 176
                                                                                                                                                                                   SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Piwnica-Worms, Helen
TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1
TITLE OF INVENTION: KINASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILING DATE: 08-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.4%; Score 649.5; DB 2; 51.6%; Pred. No. 3.2e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSE: Greenlee, Winner and Sullivan,
S: 5370 Manhattan Circle, Suite 201
Boulder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80303
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08677298
Patent No. 5863729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INPORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 729 amino acids
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Best Local Similarity 51.6'
Matches 131; Conservative
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MOLECULE TYE
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                                                                                                                                                                                                                                                                                                                                                                                          Length 631;
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APPLICANT: Bird, Timothy A.
APPLICANT: Wirca, G. Duke
APPLICANT: Wirca, G. Duke
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REFERENCE: 2923-B
CURRENT APPLICATION NUMBER: US/10/355,975A
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                               APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Wirca, G. Duke
APPLICANT: Wartin, Unja
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REPERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEC ID NOS: 36
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1342; DB 4;
; Pred. No. 7.7e-130;
0; Mismatches 0;
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Best Local Similarity 100
Matches 253; Conservative
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CRGANISM: Mus musculus
US-09-579-664B-11
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Patent No. 6514719
GENERAL INFORMATION:
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48.2%; Score 647.5; DB 4;
Best Local Similarity 51.2%; Pred. No. 5.1e-58;
Matches 130; Conservative 44; Mismatches 77;
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                                                                                                                                             Query Match

48.2%; Score 647.5; DB 4
Best Local Similarity 51.2%; Pred. No. 5.1e-58;
Matches 130; Conservative 44; Mismatches 77
               NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
 2001-10-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGTLEQIMKDRWMN 305
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                                                                                             ; ORGANISM: Rattus norvegicus
US-09-984-890-4
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 4
                                                             LENGTH: 722
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                                                                                TYPE: PRT
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Patent No. 6492156

GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

TITLE OF LINVENTION: THEREOF

FILE REFERENCE: CL001306

CURRENT APPLICATION NUMBER: US/09/984,890
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                              235 DVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPPYMSTDCENLLKRFLVLNPIK 294
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OTHER INFORMATION: GenBank Accession No. 6458561 g3089349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.4%; Score 649.5; DB 4;
51.6%; Pred. No. 3.2e-58;
tive 42; Mismatches 78;
                                                                                                                                                                                                                                    APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Molteni, Angela
APPLICANT: Magnaghi, Paola
APPLICANT: Bosorti, Roberta
APPLICANT: Scacheri, Emanuela
APPLICANT: Isacchi, Antonella
APPLICANT: Hodgson, Dave
TITLE OF INVENTION: HUMAN NIMI KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
                                                                                                                                                                          5-09-523-849-33
Sequence 33, Application US/09523849
Patent No. 645851
GENERAL INFORMATION:
                                                                                                           295 RGTLEQIMKDRWIN 308
                                                                            RATLEDVASHWWVN 252
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 729
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US-09-984-890-4
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Sequence 4, Application US/10274194

Batent No. 6706511

CENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLO01306DIV

CURRENT APPLICATION NUMBER: US/10/274,194

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEC ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0
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Length 722;
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Sequence 2, Application US/09984890

Patent No. 6492156

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001306
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTMARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                    ; LOCATION: (0)...(0)
... OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022
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48.2%; Score 646.5; DB 4;
Best Local Similarity 51.6%; Pred. No. 6.3e-58;
Matches 131; Conservative 41; Mismatches 79;
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48.2%; Score 646.5; DB 4;
Best Local Similarity 50.8%; Pred. No. 6.4e-58;
Matches 129; Conservative 45; Mismatches 77;
                 CuraPatSegFormatter Version 0.9
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NUMBER OF SEQ ID NOS: 1387
                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                NAME/KEY: misc feature
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ORGANISM: Homo sapiens
               SOFTWARE: Cure
SEQ ID NO 1022
                                                         LENGTH: 713
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Patent No. 6753314

GRUERAL INPORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REPERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2006-03-29
PRIOR PRILING DATE: 1999-04-01
PRIOR PLILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
) OTHER INFORMATION: Genbank Accession No. 6458561 g1749794
US-09-523-849-36
                                                                                                                                                                                                                     APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Molteni, Angela
APPLICANT: Bandman, Paola
APPLICANT: Bocchi, Paola
APPLICANT: Bacchi, Emanuela
APPLICANT: Isacchi, Antonella
APPLICANT: Hodgson, Dave
TITLE OF INVENTION: HUMAN NIMI KINASE
FILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT FILING DATE: 200-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL Program
                                                                                                                                                             Sequence 36, Application US/09523849
Patent No. 6458561
                                       | | | | : | : | 305
292. RGTLEQIMKDRWMN | 305
           239 RATLEDVASHWWVN 252
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ORGANISM: Homo sapiens
                                                                                                                                                                                                     GENERAL INFORMATION:
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US-09-538-092-1022
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APPLICANT: YAN, Chunhua et al.
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01306DIV
CURRENT APPLICATION NUMBER: US/10/274,194
CURRENT PILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4003-12-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTR 238
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APPLICANT: BISARO, DAVID A.
TITLE OF INFORMATION:
TITLE OF INFORMATION METHOD OF ENHANCING PLANT RESISTANCE TO PATHOGENS FILE REFERENCE: 22727-04041
CURRENT APPLICATION NUMBER: US/09/633,328B
CURRENT FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VET: 3.2
SOFTWARE: PATENTIN VET: 3.2
SEQ ID NO 2: SEQ ID NOS: 8
LENGTH: 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 724;
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50.8%; Pred. No. 6.4e-58;
iive 45; Mismatches 77
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                                                                                                                                                                     US-10-274-194-2
; Sequence 2, Application US/10274194
; Patent No. 6706511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Arabidopsis thaliana
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                                                                   239 RATLEDVASHWWVN 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-10-274-194-2
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nes 129; Conserv
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60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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48.0%; Score 644; DB 4; Length 512; 50.8%; Pred. No. 7.1e-58;
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No. 6579691el Protein Kinase (NPK-110)
: 32
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STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPACE: PC-DOS/MS-DOS
SOPRAARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.9%; Score 642.5; DB 4; 50.8%; Pred. No. 1.7e-57;
                                          47; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
FILING DATE: 30-OCT-1995
APPLICATION NUMBER: EP 94 11 7122.5
FILING DATE: 28-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 32, Application US/08817832B
; Patent No. 6579691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MANDELKOW ECKHAICA,
TITLE OF INVENTION: NO. 657969
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
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                                            Conservative
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RITIPEIROHRW 271
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Matches 129; Conserv
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CITY: Chicago
STATE: Illinois
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US-08-817-832B-32
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                     Best Local Sim
Matches 128;
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                                                            60 YRLQKTIGKGNFAKVKLARHVLTGREVAVKIIDKTQL-NPTSLQKLFREVRIMKILNHPN 118
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; OTHER INFORMATION: GenBank Accession No. 6458561 g2052189
US-09-523-849-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.9%; Score 642.5; DB 4
51.2%; Pred. No. 1.9e-57;
Live 43; Mismatches 78
                                                                                                                                                                                                                                                       Sequence 32, Application US/09523849
Patent No. 6458561
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Magnaghi, Paola
APPLICANT: Bosotti, Roberta
APPLICANT: Scacheri, Emanuela
APPLICANT: Scacheri, Emanuela
APPLICANT: Scacheri, Emanuela
APPLICANT: Hodgson, Dave
ITILE OF INVENTION: HUWAN INI KINASE
FILE REFRERENCE: PC-009 US
CURRENT APPLICATION NUMBER: US/09/523,849
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PEEL Program
SEQ ID NO 32.
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US-09-633-328B-4
; Sequence 4, Application US/09633328B
; Batent No. 6777587
; GENERAL INFORMATION:
                                                                                                                                                            239 RATLEDVASHWWVN 252
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RGSLEQIMKDRWMN 312
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ORGANISM: Rattus norvegicus
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Matches 130; Conservative
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                        APPLICANT: BISARO, DAVID A.

TITLE OF INVENTION: METHOD OF ENHANCING PLANT RESISTANCE TO PATHOGENS FILE REPERENCE: 22727-04041

CURRENT APPLICATION NUMBER: US/09/633,328B

CURRENT FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 60/147,613

PRIOR FILING DATE: 1999-08-06

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTIN VET: 3.2

SEQ ID NO 4
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47.0%; Score 631; DB 4;
Best Local Similarity 49.6%; Pred. No. 1.6e-56;
Matches 125; Conservative 48; Mismatches 77,
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ORGANISM: Nicotiana benthamiana
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RMTIPEIRMHPW 270
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January 22, 2005, 06:22:58; Search time 63.8224 Seconds (without alignments) 1422.048 Million cell updates/sec
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1 YEFLETLGKGTYGKVKKARE..........UNPTRRATLEDVASHWWVNW
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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geneseqp1090s:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aae19885 Rat SNP1/ Aae19885 Rat SNP1/ Aae19885 Rat SNP1/ Aab5319 Human pol Abu5319 Human pol Abu5319 Human pol Ad17655 Nevel hum Ad130886 Human pro Ad125362 Human pro Ad125362 Human pro Ad125362 Human pro Ad1620172 Human PRO Ad620172 Human PRO Ad620172 Human PRO Ad620172 Human BEC Aae67847 Human BCO Aae67847 Human pro Ad638421 Human roc Ad175331 Marker ge Ad115353 Human RKR Ad419734 Human TGF Ad619574 Human TGF Ad619574 Human TGF
SUMMARIES ID	AABSOOS6 AAR19885 AAAR33360 ABAB53319 ABP63119 AAU79652 ADL3362 ADL23362 ADL23362 ADL25362 ADSP56685 AABF6685 AABF6766 AABF6766 AABF6766 AABF67684 AABF1959 ABF67451
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100.0%; Score 1342; DB 4; Length 631;

Query Match

Aae00668 Human pro Aab55239 Novel pro Ad52235 Novel pro Ad52235 Novel pro Ad52235 Novel pro Ad5434 Human neu Adf74129 Human neu Ad674129 Human neu Abb04433 Human neu Abb04433 Human neu Abg73794 Human neu Ad332125 Human neu Ad33155 Human nic Ad4931727 Human mic Ad4931727 Human mic Ad4931727 Human mic Ad4931727 Human mic Ad591727 Human mic Ad691727 Human mic Ad691727 Human mic	NTS			1.	se; MLSK-1; autoimmune disorder; inflammatory disease; tumour;							on DM;		human kinase nucleic acids useful for treating nfections, tumors, allergies, autoimmune diseases, and or suppressing immune responses.		Lymph node Stromal cell kinase 1 (MLSK-1). ating a variety of disorders listed in the n, including autoimmune disorders, allergic cell deficiencies, wound healing and burns, incisions and ulcers, periodontal, tumours and bacterial, viral or fungal	
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4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	92002	AAB50056;	9-MAR-2001	Murine Lymph	Murine; Lymph node Stromal wound healing; periodontal infection; allergy.	s musculus	WO200073468-	-DEC-2000	5-MAY-2000;	28-MAY-1999;	(IMMI) IMMI	Bird TA, Vi	; 200 SDB;	Novel murine and inflammations, in for stimulating or	laim 10; Page	The present sequent This protein is use disclosure of the stactions, myeloid tissue repair and itsue repair and disease, inflammatc	Sequence 631
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                                                                  HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
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                                                                                                                                                                                                                                                                    Rat; SNF1/AMPK-Related kinase; SNARK; enzyme; stress response; diabetes; glucose deprivation; lipid metabolism; therapy; lipoprotein disorder; hyperglycaemic; drug screening; hypoglycaemia.
                          1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                   177 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLOTFCGSPLYASPEIVNGKPYVGPEVD
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            Gaps
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    Pred. No. 2.6e-138;
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100.0%; Prea. ...
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12-MAR-2001; 2001US-0274613P.
28-MAR-2001; 2001CA-02340783.
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   Best Local
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The invention relates to an AWPK (AWP-activated protein kinase) related kinase, designated SNARK polypeptides and polynucleotides. SNARK kinase, designated SNARK polypeptides and polynucleotides stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK citimates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as in other cell types such as heart and skeletal muscles, as well as concreases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted in other insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipoprotein production leading to increased come type of disorders of lipoprotein production leading to increased administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as diabetes. SNARK activity either in vivo for therapeutic purposes. Cor in vitro, for drug screening and related investigational purposes. SNARK antagonists may be administered to increase fluel production, and decrease glucose uptake and increase levels of blood glucose in a parient configurate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            decrease glucose uptake and increase levels of blood glucose in a patier
suffering from hypoglycaemia. The present sequence is rat SNARK protein
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                                                                                                                                                                                                                                                                                                  AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polynucleotides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.
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                                                                                      Lefebvre DL;
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(ONEO-) 1149336 ONTARIO INC.
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N-PSDB; AAD31710.
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from human CDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
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                                                     gene therapy; vaccine; disease treatment; detection
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               Human cell cycle-associated protein from DKFZphtes3_7j3.
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95.7%; Pred. No. 6.5e-133;
iive 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                                              (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 943; 1095pp; English.
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Best Local Similarity 95.77
Matches 242; Conservative
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                                                                                                                                       WO200112659-A2
                                                                                                                                                                                                                                                                18-AUG-1999;
28-SEP-1999;
                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       Wiemann S;
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                                                            Human;
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ABP69116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for Synthesising the full length cDNA are useful length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length not form part of the invention. Note: The sequence data for this patent did form at directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172
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                                                                                                                                                                                                                                                                                                                                                                                                                                 830 Primers useful for synthesizing full length cDNA clones and their use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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T, Koga I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 2919; 1380pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                        Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S,
Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1293; DB 4;
Pred. No. 6.5e-133;
6; Mismatches 5;
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
                                                                                                                                       07-JUL-2000; 2000EP-00114089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       in genetic manipulation.
                                                                                                                                                                                                                                                                (HELI-) HELIX RES INST
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 628 AA;
                   Homo sapiens.
                                                       EP1130094-A2
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Matches

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ABU53319

232

112

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Gape

SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA

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multiple sclerosis; diabetes; genetic disorder; wound; burn; infection, arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, into immune, genetic, myeloid or lymphoid, or platelet
                                     gene therapy; food supplement; virus; fungus;
                                    Human, genome mapping, gene therapy, food supplement, virus, fungus cell-proliferative disorder, neurodegenerative disease, bacterial, Parkinson's disease, Alzheimer's disease, autoimmune disease,
                                                                                                                                                                                                                                                                                                          Zhao QA, R'
, Ghosh M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 9; SEQ ID NO 1163; 1012pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                         odrich RW, Asundi V, Zhang J, Zł
Y, Yamazaki V, Chen R, Wang Z,
Wang D, Drmanac RT;
            ID NO 1163
                                                                                                                                                                                                                                                                                                           Goodrich RW,
                                                                                                                                                                                                                               05-MAR-2002; 2002WO-US005095.
                                                                                                                                                                                                                                                        05-MAR-2001; 2001US-00,799451.
                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation disorders.
          polypeptide SEQ
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Xue AJ, Yang Y, Ma
Wehrman T, Wang J,
                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-759812/82.
N-PSDB; ABZ11333.
                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                                                                                                                                                                             WO200270539-A2
                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                      12-SEP-2002
          Human
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Ren F;

The invention relates to an isolated polynuclectide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ1066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The cacoded polypeptides (ABR68902-ABR68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cellimaging, and places, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed appecification, but was obtained in electronic format fcation, but was obtained in electronic format
ftp.wipo.int/pub/published\_pct\_sequences

Claim 19, Fig 1, 115pp, English.

disorders.

61 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120 53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 1 YEPLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI Gaps .; 0 96.3%; Score 1293; DB 5; Length 628; 95.7%; Pred. No. 6.5e-133; 1ye 6; Mismatches 5; Indels Conservative Best Local Similarity Matches 242; Conser Query Match 윱 ò

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HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180 IAIHEVFENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVV 113

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(1) Human, protein kinase 3700, PK; protein phosphorylation, tumourigenesis, cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma; tissue repair, tissue regeneration, atherosclerosis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia; SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNFTRRA 292 for Use of modulators of activity of 3700 protein for making medicament fe.g., modulating protein phosphorylation or cell signaling, or for treating or preventing cellular proliferative and/or differentiative cytostatic; antiatherosclerotic; enzyme AAU79652 standard; protein; 628 AA. 25-SEP-2001; 2001WO-US030115. 25-SEP-2000; 2000US-0234922P. (MILL-) MILLENNIUM PHARM INC. 241 TLEDVASHWWVNW 253 TLEDVASHWWVNW 305 (first entry) Human protein kinase 3700 Galvin KM; WPI; 2002-352007/38 N-PSDB; ABK14000 WO200224921-A2. 02-JUL-2002 Curtis RAJ, 28-MAR-2002 233 AAU79652; AAU79652 ID AAU7 RESULT 6 셤 g à

The present invention relates to the isolation of a novel human protein kinase designated 3700, and the polynucleotide sequence encoding it. The invention also describes the use of a modulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a substrate protein Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylation, cell signalling, tumourigenesis, mitogenesis, transcription of a gene, angiogenesis, tissue repair, tissue repearation, esteablishment or progression of atherosclerosis, and signalling across the blood-brain progression of atherosclerosis, and signalling across the blood-brain parrier. The polynucleotide and polypeptide molecules for protein kinase 3700 may be used as diagnostic targets and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating, or curing PK-related disorders and cellular proliferative and/or carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700 polynucleotide sequence can be used to express protein kinase 3700, to detect a genetic alteration in a 3700 gene, in chromosome mapping, for tissue typing, in forensic biology, and as surrogate markers. The present

Sequence 628 AA;

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                                                                                                                 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
                                                                                                                                  HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
                                                                                                                                                                                                                                                   This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic
                                                                                                                                                                                          1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                           New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or diabeces mellitus.
                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; oytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
96.3%; Score 1293; DB 5; Length 628;
.larity 95.7%; Pred. No. 6.5e-133;
Conservative 6; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                             ADF76965 standard; protein; 628
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, Wu TD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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               1 Similarity
242; Conserv
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   Query Match
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factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the
                                                                                                                                                                                                                                                                                                                                                                                                      120
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Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga
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                                                                                                                                                                                                                                                                         Score 1293; DB 7;
Pred. No. 6.5e-133;
6; Mismatches 5;
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2000JP-00183865.
2000EP-00114089.
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Best Local Similarity 95.7
Matches 242; Conservative
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02-MAY-2000;
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Suzuki A;
                                                                                     teleangiectasia.
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   Esumi H,
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                                                                                            This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins intra associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
                                                                                                                                                                                                                                                                                                                                                      SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 112
                                                                                                                                                                                                                                                                                                                                         IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
                                                                                                                                                                                                                                                                                                                                                                                        HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                         YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEODLLHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                     Gaps
                                    primers (830 cDNAs) useful for synthesizing full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic, Neuroprotective, Nootropic, Muscular, Gene therapy, Adenosine Monophosphate activated Protein Kinase-related kinase 5, AMPK-related kinase 5, AMPK-related kinase 5, AMR5, KIAA0537, stress resistance, tumour, nervous disorder, muscle disorder, ataxia teleangiectasia, SNARK.
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                                                                                                                                                                                                                                             Length 628;
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2
                                                                                                                                                                                                                                          Score 1293; DB 8;
Pred. No. 6.5e-133;
6; Mismatches 5;
                                                                       Example 1; SEQ ID NO 2919; 1340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NINA-) JAPAN AGENCY NAT INST HEALTH. (PHAR-) ORG PHARM SAFETY & RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL25362 standard; protein; 628
                                                                                                                                                                                                                                            96.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLEDVASHWWVNW 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.77
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEO ID 12
 WPI; 2004-204755/20.
                                   New oligonucleotide
length human cDNAs.
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            N-PSDB; ADL30885
                                                                                                                                                                                                                     Sequence 628 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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The present invention relates to human Adenosine Monophosphate activated Protein Kinase (AMPK)-related kinase 5 (ARK5/ KIAA0537) and its coding sequence, which are useful for imparting stress resistance to cells. ARK5 is useful for treatment and prevention of tumours, nervous disorders, muscle disorders and ataxia telebanglectasia. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRDLKLENILLLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMYNPTRRA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective; nephrotropic; antibiproid; dermatological; immunomodilator; cell proliferation disorder; cell differentiation disorder; brain disorder; cell differentiation disorder; brain disorder; platelet disorder; breast disorder; colon disorder; kidney disorder; renal disorder; lung disorder; colon disorder; prostate disorder; cervical disorder; spleen disorder; thymus disorder; thyroid disorder; testes disorder; haematopoietic disorder;
                                                          Agent for imparting stress resistance to cells, comprises DNA encoding for adenosine monophosphate activated protein kinase-related kinase 5 itreatment of tumors, muscle and nervous disorders, and ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96.3%; Score 1293; DB 8;
95.7%; Pred. No. 6.5e-133;
live 6; Mismatches 5;
                                                                                                                                                                                                              Example 1; SEQ ID NO 12; 143pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human gene 3700 encoded protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 TLEDVASHWWVNW 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLEDVASHWWVNW
WPI; 2004-248195/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 628 AA;
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New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1988, m1983, 38555 or 593 nucleic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, or a subject at risk of developing a disorder, which is
multiple sclerosis; Crohn's disease; psoriasis; asthma;
cell proliferation; cell differentiation; cell growth; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rudolph-Owen LA;
Chun M, Williamson MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meyers RE,
Galvin KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; SEQ ID NO 44; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kapeller-Libermann R, Hunter JJ,
Curtis RAJ, Olandt PJ, Tsai F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001; 2001US-00920346.
13-AUG-2001; 2001US-00928531.
14-AUG-2001; 2001US-00929218.
15-AUG-2001; 2001US-0312539P.
25-SEP-2001; 2001US-0312539P.
08-NOV-2001; 2001US-00008016.
                                                                                                                                                               98US-00163821.

99US-017580P

99US-00276400.

99US-00392189.

99US-00412210.

99US-00412210.

99US-00412210.

2000US-020648P

2000US-020648P

2000US-020648P

2000US-020648P

2000US-020648P

2000US-020668P

2000US-021928P

2000US-021928P

2000US-024669P

2000US-024669P

2000US-0248833P

2000US-026048

2000US-026048

2000US-02757511P

2001US-00909343.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-00003690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JAN-2003; 2003US-00336489
03-JAN-2003; 2003US-00336153
                                                                                                                                       2003US-00423543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heart failure and angina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olandt PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-268788/25
                                                                                US2004058355-A1.
                                                                                                                                                                                                                                                                                                                                             25-SEP-2000; 2
08-NOV-2000; 2
09-NOV-2000; 2
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15-NOV-2000; 2
22-DEC-2000; 3
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27-APR-2001;
                                                        Homo sapiens.
                                                                                                                                       25-APR-2003;
                                                                                                                                                                                                                                                                                         19-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-NOV-2001;
                                                                                                           25-MAR-2004
                            human.
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assection accorder, 26443, 50549, 30949, 2094, 1, 2094, 1, 1904, 2001, 1000, 21529, 26176, 26443, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 activity, such as cellular proliferative and/or differentiative disorders, brain disorders, platelet disorders, breast disorders, colon disorders, kidney (renal) disorders, lung disorders, prostate disorders, tentes disorders, covarian disorders, thyroid disorders, testes disorders, chamalogical cisorders, disorders, cardiovascular disorders, conductors, disorders, askeletal muscle disorders, skin (dermal) disorders, disorders, associated with bone metabolism, canducted; endothelial cell disorders, liver disorders, viral diseases, pain disorders, liver disorders, viral diseases, pain cisorders, liver disorders, viral diseases, pain disorders, liver disorders, respectives or angiogenic disorders exploradisorders, heart failure, hypertension, candina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease, psoriasis, or asthma. The nucleic acid molecules and canductors of disease, psoriasis, or asthma. The nucleic acid molecules and canductors of disease, soriasis, or asthma. The nucleic acid molecules and canductors of disease, soriasis, or asthma. The nucleic dispersed of division, growth and cid vision. This is the amino acid sequence of a novel human process, condivision, many and a series of division. This is the amino acid sequence of a novel human procession of the convertion where the convertion is the convertion of convertion and convertions and con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention. Note: The sequences given in the specification are also avaialable in electronic format from ftp. seqdata.uspto.gov/sequence.html?DocID=2004058355.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.3%; Score 1293; DB 8; Length 628; 95.7%; Pred. No. 6.5e-133;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Mismatches
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Best Local Similarity
Matches 242; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 628 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
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Claim 1; SEQ ID NO 77; 366pp; English.
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                                                                                                                                              15-JUL-2003; 2003WO-US021730
                                                                                                                                                                      15-JUL-2002; 2002US-0395632P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.38;
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Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLEDVASHWWVNW
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                                                                                                                                                                                                                     Manning G,
                                                                                                                                                                                                                                            WPI; 2004-122753/12
                                                                                                                                                                                              (SUGE-) SUGEN INC
                                                                                                                                                                                                                                                      N-PSDB; ADJ96554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 672 AA;
                                                                                                WO2004006838-A2
                                                               sapiens
                                                                                                                      22-JAN-2004
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                                      Nua<sub>K2</sub>
                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAIHEVFENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVV 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSFLYASFEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 292
                                                                                                                                                                  Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human calcium/calmodulin-dependent protein kinase NuaK2 protein SeqID 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase; human; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease;
                                                                                                                                                                                                                                                 The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthitis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                          polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  96.3%; Score 1293; DB 8; Length 628;
llarity 95.7%; Pred. No. 6.5e-133;
Conservative 6; Mismatches 5; Indels
                                                                                             Schoenfeld J,
                                                                                                                                                                                                                            Claim 7; SEQ ID NO 1080; 1731pp; English.
                                                                                               Chiu H,
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                                                                                            Dennis K, Clark H,
Wu TD;
                       06-NOV-2003; 2003WO-US035268
                                               08-NOV-2002; 2002US-0425235P
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                                                                       (GETH ) GENENTECH INC
                                                                                                                                                                                                        spondyloarthropathy.
                                                                                                                               WPI; 2004-420067/39.
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Matches 242; Conserv
                                                                                                                                             N-PSDB; ADO20171
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 628 AA;
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                                                                                             Fong S, I
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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (FTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antilinflammatory activities. This polypeptide sequence is a human kinase protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
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cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroprotective; immunomodulator; antiinflammatory; enzyme; calcium/calmodulin-dependent protein kinase;
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Pred. No. 7.2e-133;
6; Mismatches 5;
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Human; kinase; PKIN-12; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; ALDS Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mollitus; osteoarthritis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; cardiovascular disease; hypertension; vasculitis; angina pectoris; congestive heart failure; ischemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy.
                                                                                                                                                                                                                          "Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                    23. .260
/label= Protein_kinase_domain
                                                                                                                                                                                                                                                                      24. .260
/label= Protein_kinase_domain
                                                                                                                                                                                                                                            /label= Protein_kinase_domain
                                                                                                                                                                                                       Location/Qualifiers
                                             Human kinase PKIN-12 protein.
                                                                                                                                                                                                                                                                                                                                          14-JUN-2001; 2001WO-US019444
                            (first entry)
                                                                                                                                                                                                                                  .260
                                                                                                                                                                                                                 19. .269
/note= "E
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                            26-MAR-2002
                                                                                                                                                                                   Homo sapiens
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         AAE16266;
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## 15-JUN-2000; 2000US-0212073P. 23-JUN-2000; 2000US-0213467P. 30-JUN-2000; 2000US-0216651P. 07-JUL-2000; 2000US-0216605P. 13-JUL-2000; 2000US-021865P. 25-AUG-2000; 2000US-0228056P.

Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

(INCY-) INCYTE GENOMICS INC.

WPI; 2002-090207/12. N-PSDB; AAD26459. polypeptides, useful for diagnosing, treating or preventing disorders growth and development, cardiovascular and lipid, and diseases such as of growth and development, cardiovascular a cancer, comprise human kinase polypeptides.

Claim 1; Page 152-153; 197pp; English

The invention relates to human kinase PXIN proteins and their corresponding cDNAs. A composition containing PXIN agonist is useful for treating a disease or condition associated with decreased expression of PXIN and a composition comprising PXIN antagonist is useful for treating a disease or condition comprising PXIN antagonist is useful for treating a disease or condition associated with overexpression of PXIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, tratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atheroselerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, disease, mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,

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rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts; cardio vascular disease (arteriovenous fistula, hypertension, vasculitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, ischaemic heart disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human
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                                                                                                                                                                                                                                                                                                                                        9
syndrome,
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                                                                                                                                                                                                                                                                                                                                        1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
osteoporosis, pancreatitis, psoriasis, Reiter's
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0
                                                                                                                                                                                                                                                                      Length 594;
                                                                                                                                                                                                                                                                95.8%; Score 1286; DB 5;
95.3%; Pred. No. 3.5e-132;
live 6; Mismatches 6;
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 95.3'
                                                                                                                                                                                                                                   Sequence 594 AA;
 osteoarthritis,
                                                                                                                                                                                                PKIN-12 protein
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ABP96085 standard; protein; 611 07-MAY-2003 (first entry) ABP96085; 

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Human protein kinase SEQ ID NO:76.

Human; protein kinase; enzyme; antiasthmatic; antiinflammatory; antidabatic; antiparkinsonian; antimigranie; cardiant; cytostatic; immunosuppressive; vulnerary; gene therapy; COPD; asthma; migraine; chronic obstructive pulmonary disease; non-insulin dependent diabetes; Parkinson's disease; myocardial infarction; inflammatory bowel disease; autoimmune disorder; allograft rejection; inflammatory bowel disease; cancer; leukaemia; wound granulation.

Homo sapiens

WO2003000901-A2 03-JAN-2003 24-JUN-2002; 2002WO-IB002358

26-JUN-2001; 2001US-0301098P 06-NOV-2001; 2001US-0332870P

(DECO-) DECODE GENETICS EHF.

Sigurdsson GT Martinez RAM,

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ABZ77126 to ABZ77165 encode the human protein kinases given in ABP96048 to ABP96087. The protein kinases have antiasthmatic, antiinflammatory, amridiabetic, antiparkinsonian, antimigrafine, cardiant, cytostatic, immunosuppressive and vulnerary activities, and can be used in gene therapy. A protein kinase therapeutic agent from the present invention, particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers (e.g. leukaemias) or wound granulation
                                                                            New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction, allograft rejection
                                                                                                                                                                                                         Claim 9; Page 87; 258pp; English
                                                                         protein kinase
                        N-PSDB; ABZ77163
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Sequence 611 AA;

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YEFLETIGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI 112
                                                                                                                 61 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
                                                                                                                                    HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                  SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPS-----DACGLIRWLLM 233
                                                                                                                                                                                                                                                    HEDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVD
                                                         1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIBIMSSLNHPHI
                              7;
 Length 611;
                               5; Indels
 DB 6;
95.3%; Score 1279.5; DB 6
93.1%; Pred. No. 1.9e-131;
ive 6; Mismatches 5;
                                                                                                                                                                                                                                                                                                               VNPTRRATLEDVASHWWVNW 312
                                                                                                                                                                                                                                                                                           VNPTRRATLEDVASHWWVNW
                            Matches 242; Conservative
                Local Similarity
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protein kinase, SEQ ID NO: 159.
AAB65632 standard; protein; 629
               (first entry)
               27-MAR-2001
       AAB65632;
                      Novel
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Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatrological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.

Homo sapiens

40200073469-A2

07-DEC-2000

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The present sequence is a novel protein kinase. The novel protein kinases, and the nucleic acids that encode them may be used in the treatment and diagnosis of disasses associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Diseases related to kinase antibodies expression and activity. Diseases related to kinase expression and activity. Diseases related to kinase autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, processis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 SWSLGVLLYILVHGTWPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 IAIHEVFENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIVSAVHYCHQNRVV 172
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                                                                                                                                                                                                                                  Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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                                                                                                                              Sudersanam S;
                                                                                                                                                                                                                                                                             neurodegenerative diseases and/or cancers
                                                                                                                            Whyte D,
                                                                                                                                                                                                                                                                                                                     Claim 10; Fig 1; 310pp; English
26-MAY-2000; 2000WO-US014842.
                                          99US-0136503P
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                                                                                                                              Martinez
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N-PSDB; AAF44659.
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                                                                                    (SUGE-) SUGEN
                                          28-MAY-1999;
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Search completed: January 22, 2005, 06:38:27 Job time : 64.8224 secs

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January 22, 2005, 06:43:09; Search time 58.6708 Seconds (without alignments) 1557.950 Million cell updates/sec
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1 YEFLETLGKGTYGKVKKARE.........VNPTRRATLEDVASHWWVNW 253
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1: \cgn2_6/ptodata/1/pubpaa/PCT_PBECOMB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PCT_PBEW_PUBL-pep:*

3: \cgn2_6/ptodata/1/pubpaa/PCT_BW_PUBL-pep:*

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9: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

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16: \cgn2_6/ptodata/1/pubpaa/USIOD_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	Sequence 11, Appl	Sequence 103, App	Sequence 41, Appl	Sequence 50, Appl	Sequence 2, Appli	Sequence 44, Appl	Sequence 640, App	Sequence 77, Appl	Sequence 12, Appl	Sequence 101, App	Sequence 23, Appl	Sequence 26, Appl	Sequence 2, Appli
		ID	US-10-355-975-11	US-10-343-514-103	US-10-343-514-41	US-10-343-514-50	US-09-963-159-2	US-10-423-543-44	US-10-370-715B-640	US-10-618-941-77	US-10-311-034-12	US-10-343-514-101	US-10-322-281-23	US-10-322-281-26	US-09-780-949-2
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; TYPE: PRT
; ORGANISM: RAT
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Sequence 103, Application US/10343514

Bellication No. US20040132025A1

GENERAL INFORMATION:
APPLICANT: BOESEN, Cheryl F.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: ROSEN, Cheryl F.
TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: Diana L.
TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DA-DHUCZ/PCT
CURRENT APPLICATION NUMBER: US/10/13/3,514

CURRENT FILING DATE: 2003-01-31

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0
                                                                         181 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                         237 SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 296
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Publication No. US20040132025A1
GENERAL INFORMATION:
APPLICANT: DRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
                                                                                                                                                                             241 TLEDVASHWWVNW 253
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; ORGANISM: Homo sapiens
US-10-343-514-103
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APPLICANT: LEFEBVRE, Diana L.

TITLE OF INVENTION: AMPK.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUGZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514

CURRENT FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/22,650

PRIOR PELING DATE: 2001-08-02

PRIOR FILING DATE: 2001-08-08

PRIOR FILING DATE: 2001-03-12

PRIOR PELING DATE: 2001-03-28

PRIOR APPLICATION NUMBER: CA 2,340,780

PRIOR PELING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PALENTIN VERSION 3.0

SEQ ID NO 41

LENGTH: 630
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Publication No. US20040132025A1

GENERAL INFORMATION:
APPLICANT: DRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: LEFEBVER, Daniel J.
APPLICANT: LOSEN, Cheryl F.
CURRENT APPLICATION NUMBER: US/10/343,514
CURRENT APPLICATION NUMBER: US/10/343,514
FRIOR APPLICATION NUMBER: US 60/222,650
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 109
SEQ ID NO 50
SEQ ID NO 50
LENGTH: 251
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Pred. No. 2e-97;
3; Mismatches 2; Indels 0
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Best Local Similarity 98.0%;
Matches 248; Conservative
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; ORGANISM: RAT
US-10-343-514-50
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the stanta property

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US-09-963-159-2
US-09-963-159-2
i Sequence 2, Application US/09963159
i Patent No. US20020077312A1
i GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR FILE REFERENCE: 10147-5001.
CURRENT APPLICATION NUMBER: US/09/963,159
CURRENT FILING DATE: 2001-09-25
i PRIOR PILING DATE: 2000-09-25
i NUMBER OF SEQ ID NOS: 3
i SOFTWARE: PatentIn Ver. 2.1
i SEQ ID NO 2
i TYPE: PRT
i TYPE: PRT
i ORGANISM: Homo sapiens
US-09-963-159-2
                                                                                                                  61 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
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                                                            1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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Length 251;
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                              Indels
Query Match 96.6%; Score 1296; DB 16; Best Local Similarity 98.0%; Pred. No. 1.7e-96; Matches 246; Conservative 3; Mismatches 2;
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Sequence 44, Application US/10423543; Publication No. US20040058355A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo Sapiens
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Length 672; Indele

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61 IAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIV 120
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                                                                                                                                                                                                                 97 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLMHIRREIEIMSSLNHPHI
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                                                                                                         Score 1293; DB 17;
Pred. No. 9e-96;
6; Mismatches 5;
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Publication No. US20040023242A1
GENERAL INFORMATION:
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APPLICANT: ELLICYT, Vicki S.
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajeev
APPLICANT: ISON, Craig H.
APPLICANT: SAO, FRANCE, FILE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LU, Yan
GANDHI, Ameena R.
TRIBOULEY, Catherine M
CHAWLA, Narinder K.
YAO, Monique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
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GURURAJAN, Rajagopal
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GRIFFIN, Jennifer A.
KEARNEY, Liam
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POLICKY, Jennifer L
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RECIPON, Shirley A.
                                                                                                         Query Match
Best Local Similarity 95.7%;
Matches 242; Conservative
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BOROWSKY, Mark L.
AU-YOUNG, Janice
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THORNTON, Michael
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LAL, Preeti
                     TYPE: PRT
CRGANISM: Homo sapiens
US-10-618-941-77
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    LENGIH: 672
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APPLICANT: BODARY, SARAH C.

APPLICANT: BODARY, SARAH C.

APPLICANT: BULLARY

APPLICANT: BRISDELL, HUNTE

APPLICANT: JACKMAN, JANET

APPLICANT: SCHORNFELD, JILL R.

APPLICANT: WOLD, WILLIAM, P. MICKEY

APPLICANT: WOOD, WILLIAM I.

APPLICANT: WO, THOMAS D.

TITLE OF INVENTION: Related Diseases

FILE REFERENCE: P1948R.US

FILE REFERENCE: P1948R.US

CURRENT APPLICATION NUMBER: US/10/370,715B

CURRENT FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 742

SEQ ID NO 640

LENGHH: 628

***CHARTH: 628
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Pred. No. 8.4e-96;
6; Mismatches 5;
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Sequence 77, Application US/10618941
Bublication No. US20040197792A1
GENERAL INFORMATION:
APPLICANT: WANNING, GERAED
APPLICANT: CARENPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION UNDHER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR PILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 77
                                                                                                                                         Sequence 640, Application US/10370715B Publication No. US20040258678A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.3%;
95.7%;
241 TLEDVASHWWVNW 253
                       TLEDVASHWWVNW 305
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Best Local Similarity 95.7
Matches 242; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-640
                                                                                                                    US-10-370-715B-640
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                                            1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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Publication No. US20040126/62A1

GENERAL INFORMATION:

JAPLICANT: David W. Morris

APPLICANT: Marc S. Malandro

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE 5.29452001000

CURRENT APPLICATION NUMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 640
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94.9%; Score 1273; DB 16;
Best Local Similarity 97.2%; Pred. No. 3.5e-94;
Matches 246; Conservative 0; Mismatches 1;
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US-10-322-281-26
Sequence 26, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TLEDVASHWWVNW 253
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ORGANISM: Mus musculus
US-10-322-281-23
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CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
60/228,056
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-05-07-13; 2000-06-07-13; 2000-06-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-07-13; 2000-
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Publication No. US20040132025A1

Sequence 101, Application US/10343514

Publication No. US20040132025A1

APPLICANT: DRUCKER, Cheryl F.

APPLICANT: LEFEBNE, Diana L.

TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK

FILE REPERENCE: DPA-DRUCZ/PCT

CURRENT APPLICATION NUMBER: US/10/343,514

CURRENT APPLICATION NUMBER: US/10/343,514

CURRENT APPLICATION NUMBER: US/01/01109

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2001-03-12

PRIOR PELING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SEQ ID NO 101

LENGTH: 251

TANDER OF SEC ID NOS: 109

SEQ ID NO 101

LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 HRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRA 240
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                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CD1
US-10-311-034-12
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Best Local Similarity 95.6
Matches 240; Conservative
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60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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                                                                                                                  180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
                                                                                        180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
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| Sequence 6, Application US/09780949
| Patent No. US20020006618A1
| Patent No. US20020006618A1
| Patent No. US20020006618A1
| Patent No. US20020006618A1
| APPLICANT: Kapeller-Liberman, Rosana
| APPLICANT: Weich, Nadine S.
| APPLICANT: Weich, Nadine S.
| TITLE OF INVENTION: Methods for Using 20893, a Human Protein
| TITLE OF INVENTION: Methods for Using 20893, a Human Protein
| TITLE OF INVENTION: Minase
| TITLE OF INVENTION: WINBER: US/09/780,949
| CURRENT APPLICATION NUMBER: US 60/181,690
| PRIOR FILING DATE: 2000-02-09
| NUMBER OF SEQ ID NOS: 6
| SEQ ID NO 6
| SEQ ID NO 6
| LEAST SEQ ID NO 6

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84.1%; Score 1128.5; DB 9; Length 661;

Best Local Similarity 82.3%; Pred. No. 1.6e-82;

Matches 209; Conservative 24; Mismatches 20; Indels 1;
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Publication No. US20030157082A1
GENERAL INFORMATION
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: MascBeth, Kyle J.
APPLICANT: Hunter, John Joseph
APPLICANT: Tsai, Fong-Ying
APPLICANT: Lescon, Andrea
APPLICANT: Lightcap, Bric S.
APPLICANT: Williamson, Mark
APPLICANT: Williamson, Mark
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| ATIEDIANHWWVNW 308
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295 ATIEDIANHWWNW 308
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US-09-780-949-6
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US-09-780-949-6
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APPLICANT: Waich, Nadine S.
APPLICANT: Galvin, Katherine M.
TITLE OF INVENTION: Methods for Using 20893, a Human Protein
TITLE OF INVENTION: Kinase
FILE REFERENCE: 035800/209015
CURRENT APPLICATION NUMBER: US/09/780,949
CURRENT FILING DATE: 2001-02-09
PRIOR PLILAGION NUMBER: US 60/181,690
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 2
LENGTH: 661
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                                                                                                                                                                                                                                                                                                                                            Length 616;
  TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 202-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                            Score 1230; DB 16
Pred. No. 9.8e-91;
6; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 2, Application US/09780949; Patent No. US20020006618A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 TLEDVASHWWVNW 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLEDVASHWWVNW 299
                                                                                                                                                                                                                                                                                                                                               Query Match 91.7
Best Local Similarity 93.3
Matches 236; Conservative
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                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: H. sapiens
US-09-780-949-2
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                                                                                                                                                                                                                                                                                          US-10-322-281-26
                                                                                                                                                                                                          LENGTH: 616
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                                                                                                                                                                             SEQ ID NO 26
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Best Local S:
Matches 209
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239

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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 7481, 7660, 2541, 69581, 4969, 11682, 1767, 2535,
TITLE OF INVENTION: 7181, 7660, 2541, 69581, 4969, 11682, 1767, 2535,
TITLE OF INVENTION: 3703, 14171, 1039, 1660, 1450, 18894, 2088, 33427, 2160,
TITLE OF INVENTION: 3703, 14171, 1039, 1660, 1450, 18894, 2088, 33427, 2160,
TITLE OF INVENTION: 8990, 2100, 9286, 64689, 1684, 26857, 1844, 9552, 1444, 4669,
TITLE OF INVENTION: 8990, 2100, 9286, 46681, 1840, 2893, 33230, 1566, 9943,
TITLE OF INVENTION: 2150, 26883, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
TITLE OF INVENTION: 2150, 26883, 2011, 14031, 6178, 21225, 1420, 3226, 2099,
TITLE OF INVENTION: 2150, 26883, 2011, 14031, 6178, 21225, 1420, 3226, 2099,
TITLE OF INVENTION: 2150, 26883, 2011, 14031, 6178, 21225, 1420, 3226, 2099,
FRIOR FALING DATE: 2002-01-31
PRIOR FADELICATION NUMBER: US 60/331, 075
PRIOR FLING DATE: 2002-04-16
PRIOR PRIOR PLING DATE: 2002-04-16
PRIOR PLING D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 DSWALGVLYTLVYGTMPFDGFDHKNLIRQISSGEYREPTQPSDARGLIRWMLMVNPDRR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YEFLETLGKGTYGKVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.1%; Score 1128.5; DB 14; Length 661;
82.3%; Pred. No. 1.6e-82;
ive 24; Mismatches 20; Indels 1;
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ne : 59.6708 secs
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ATIEDIANHWWVNW 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 82.3
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 661
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Job time
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

January 22, 2005, 06:29:16; Search time 15.4548 Seconds (without alignments) 1575.104 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-980-464-11\_COPY\_57\_309 1342 1 YEFLETLGKGTYGKVKKARE.........vNPTRRATLEDVASHWWVNW 253

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	hypothetical prote	serine/threonine p	probable serine/th	serine/threonine-s	probable serine/th	hypothetical prote	serine/threonine-s	serine/threonine-s	probable serine/th	probable serine/th	protein H39E23.1 [	SNF-related kinase	serine/threonine-s	probable serine/th	qik protein - chic	hypothetical prote	FOG2 protein - yea	c	[hydroxymethy]glut	[hydroxymethylglut	probable serine/th	probable carbon ca	hypothetical prote	protein kinase - m	serine/threonine p	serine/threonine-s	serine/threonine-s	SNF1-related prote	serine/threonine-s
SUMMARIES	ID	T29253	G01025	827966	T52633	T10449	T13741	JC1446	A56009	I48609	T18611	G89287	B90100	A26030	T07415	JC7500	T29858	S72513	S59941	S51025	A53621	T07788	T41587	T20941	149072	T04145	S44859	A41361	B90120	860303
	DB	5	~	7	7	~	~		7	~	~	~	~	Н	N	~	~	~	٦	-	-	7	7	7	7	7	-	7	7	7
	Length	1558	745	713	512	504	1398	512	511	774	1192	1246	472	633	504	798	262	602	473	552	552	512	576	887	481	510	622	502	401	513
æ	Query Match	9.09	48.2	œ	٠	47.8	47.6	47.5	47.0	46.8	9	46.3	46.3	46.2	46.1	46.0	45.9	45.8	45.5	45.0	44.8	44.6	44.1	43.5	43.2	43.0	42.7		•	41.8
	Score	813.5	647.5	46	644	641	638.5	637	631	N	621.5	621.5	621	619.5	618	617.5	616	614.5	610	604	601	599	591.5	583.5	579.5	576.5	573	67.	566.5	61.
	Result No.		7	М	4	ស	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

RESULT 2
G01025
serine/threonine protein kinase - human
c:Species: Homo sapiens (man)
C;Date: 21-Dec.1996 #sequence\_revision 06-Jun-1997 #text\_change 16-Aug-2004
C;Accession: G01025

serine/threonine-s	protein kinase kin	protein kinase 1 -	probable protein k	p69Eg3 protein - A	probable serine/th	probable serine/th	GIN4 protein - yea	probable serine/th	serine/threonine-s	serine/threonine-s	probable protein k	probable purine nu	probable protein k	serine/threonine-s	hypothetical prote
S60304	T40503	A38903	C84667	S52244	A86427	T14735	859359	T14736	864930	S52687	E84707	S37928	T02306	T09903	E96522
н	~	~	~	7	~	~	7	~	~	~	~	~	~	~	7
513	891	891	441	651	480	440	1142	440	1147	1064	435	1518	502	445	421
41.8	40.3	40.2	39.8	39.7	39.7	39.3	39.2	39.5	39.1	39.0	38.8	38.5	38.0	37.8	37.3
560.5	541	540	534.5	533	532.5	527.5	526	525.5	525	523	521	516	510	507.5	500.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1 T29253 hypothetica C;Species: C;Date: 15- C;Accession R;Murray, J Submitted t A;Descripti A;Reference A;Reference A;Residues; A;Residues; A;Genetics:	Derotein B0496.3 - Caenorhabditis elegans Caenorhabditis Caenorhabditis elegans Caenorhabditis Caenorhabdit	843/2; 90
Query Ma Best Loo Matches	Query Match 60.6%; Score 813.5; DB 2; Length 1558; Best Local Similarity 61.7%; Pred. No. 2.7e-27; Matches 156; Conservative 33; Mismatches 63; Indels 1; Gaps 1;	
o d	1 YEFLETLGKGTYGKVKKARESS-GRLVAIKGIRKDKIKDEQDLLHIRREIEIMSSLNHPH 59 	
රු යු	60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119     :        ::     :      :    135 IIQIYEVFENKDKIILVMEYSSGGELYDYVSRCGSLPEAEARRIFRQITSAVLYCHKHRV 194	
è q	120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179	
S d	180 DSWSLGVLLYILVHGTMPPDGQDHKTLVKQISNGAVREPPKBSDACGIJRWLLMVNPTRR 239	
O,	240 ATLEDVASHWWVN 252   :     :  315 ATIFDIASHWWLN 327	

Jan

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serine/threonine-specific protein kinase (EC 2.7.1.-) AKINI1 [validated] - Arabidopsis th
N;Alternate names: SNF1 protein kinase omolog AKINI1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated, Mt complements SNP1 mutations in yeast C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 VHRDLKPENLLLDSRCNIKIADFGLSNVMRDGHFLKTSCGSPNYAAPEVISGKLYAGPEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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A,Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable serine/threonine-specific protein kinase (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.8%; Pred. No. 1.4e-20;
Matches 128; Conservative 47; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
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RITIPEIROHRW 271
                                                                                                                                                             239 RATLEDVASHWWVN
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C;Superfamily: protein kinase homology
C;Kywordsa: ATP; phosphotransferase; Berine/threonine-specific protein kinase
F;54-307/Domain: protein kinase homology <KIN>
F;62-70/Region: protein kinase ATP-binding motif
                 R;Navarro, E.
submitted to the EMBL Data Library, April 1996
A;Reference number: H00564
A;Accession: G01025
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRWA
A;Mesiques: 1-745 «NAV»
A;Resiques: 1-745 «NAV»
A;Cross-references: UNIPROT:Q15524; UNIPROT:Q96HB3; EMBL:X97630; NID:g1310674
C;Superfamily: protein kinase homology
F;18-271/Domain: protein kinase homology
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48.2%; Score 646.5; DB 2; Length 713;
Best Local Similarity 51.6%; Pred. No. 1.4e-20;
Matches 131; Conservative 41; Mismatches 79; Indels 3
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51.2%; Pred. No. 1.3e-20;
ive 44; Mismatches 77
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Best Local Similarity 51.2<sup>3</sup>
Matches 130; Conservative
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Cispecies: Drosophila melanogaster
Cispecies: J3-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
Cispecies: J3-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
Cispecies: J4-Airis, D.; Barrell, B.
Submitted to the EMBL Data Library, April 1999
Airestription: Sequencing the distal X chromosome of Drosophila melanogaster.
Airestription: Sequencing the distal X chromosome of Drosophila melanogaster.
Airestription: 11344
Airestription: Jafetal X chromosome of Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPK-PSDACGLIRWLLMVNPTR 238
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C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidy
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                      1 YEFLETLGKGTYGKVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                      Query Match 47.8%; Score 641; DB 2; Length 504; Best Local Similarity 50.4%; Pred. No. 1.8e-20; Matches 127; Conservative 47; Mismatches 76; Indels
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RITIPEIRQHPW 259
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A; Accession: JC1446
A; Molecule type: DNA
A; References: UNIPROT: Q38997; GB: M93023; NID: g166599; PIDN: AAA32736.1; PID: g166600
R; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
Submitted to the EMBL Data Library, May 1995
A; Description: Differential accumulation of the transcripts of 22 novel protein kinase g A; Reference number: $58256
A; Accession: $58266
A; Accession: $58266
A; Residues: 144-198 < ATH
A; Residues: 144-198 < ATH
A; Residues: 144-198 < ATH
A; Residues: 148 < ATH
A; Residues: 1881.28 < ATH
A; Residues: 1881.886966; NID: g928909; PIDN: CAA60529.1; PID: g928910
R; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
A; Cross-references: EMBL: X86966; NID: g928909; PIDN: CAA60529.1; PID: g928910
A; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
A; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
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A; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
A; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
A; Thuemmler, F; Kirchner, M; Teuber, R; Dittrich, P.
A; Thuemmler, F; M; M; Dittrich, Dittrich,
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A,Residues: 144-198 <TH2>
A,Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C,Comment: This enzyme plays an important role in a signal transduction cascade regulation
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F:55-33/Region: protein kinase ATP-binding motif F:55-33/Region: protein kinase ATP-binding motif F:48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F:147,151/Binding site: magnesium (Asn, Asp) #status predicted
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serine/threonine-specific protein kinase (BC 2.7.1.-) AK21 - Arabidopsis thaliana NiAlternate names: protein kinase SNF1 homolog C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: JC1446; S58266; S66334 R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M. A;Altle: Structure and expression of a gene from Arabidopsis thaliana encoding a particle communication of the structure and expression and structure and expression of the structure and expression expre
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A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
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49.6%; Pred. No. 2.7e-20;
tive 50; Mismatches 75; Indels
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Matches 125; Conservative 5
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Length Indels

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IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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                                                                                                                                         C;Superfamily: protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P;51-304/Domain: protein kinase homology <KIN>
P;59-67/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
46.8%; Score 627.5; DB 2
Best Local Similarity 50.0%; Pred. No. 8.9e-20;
Matches 127; Conservative 44; Mismatches 8C
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A;Status: translated from GB/EMBL/DDBJ
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;Status: translated from GB/EMBL/DDBJ
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A;Cross-references: EMBL:X70764
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                                                 C,Genetics:
A,Gene: emk
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C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
C.Accession: 148609; S31333
R.Inglis, J.D.; Lee, M.; Hill, R.E.
Mamm. Genome 4, 401-403, 1993
A;Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome 19.
A;Reference number: 148609; MUID:93364122; PMID:8358177
A;Reference number: 148609; MUID:93364122; PMID:8358177
A;Reference number: 148609
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-74 < ING)
A;Residues: 1-74 < ING)
A;Residues: UNIPROT:Q05512; EMBL:X70764; NID:G57919; PIDN:CAA50040.1; PID:G57920
R;Inglis, J.D.; Lee, M.; Hill, R.E.
submitted to the EMBL Data Library, January 1993
A;Description: A novel protein kinase with homologues in yeast maps to mouse chromosome A;Reference number: S31333
A;Molecule type: mRNA
A;Residues: 1-698, K', 700-702, 'GRGLPTAARASCTSGTCYCAGMAHQATRT', 731-774 <ING2>
                                                                       Section to the specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco (Species Nicotiana tabacum (common tobacco) (Species Nicotiana tabacum (common tobacco) (Species Nicotiana tabacum (common tobacco) (Species Nicotiana tabacum, 1.3 Banno, H.; Machida, Y. Mol. Call. Banno, H.; Machida, Y. Mol. Call. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces certase of Saccharomyces cer
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A.Molecule type: mRNA
A.Molecule type: proper type: mRNA
A.Molecule type: proper type: pr
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A;Accession: A56009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.0%; Score 631; DB 1;
49.6%; Pred. No. 4.7e-20;
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Matches 125; Conservative
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probable serine/threonine-specific protein kinase (EC 2.7.1.-), long splice form - Caenoi Nicontains: probable serine/threonine kinase, short splice form C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans c.f. proteins: 15-0ct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Residues: 1-1192 <WIL1>
, Cross-references: UNIPROT: Q9TW45; EMBL: Z81027; PIDN: CAB54179.1; GSPDB: GN00023; CESP: H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-487,536-1192 <WIL2>
A;Cross-references: EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023; CESP:H39E23.1b
A;Experimental source: clone AH10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: i-1192 <WIL3>
A;Cross-references: EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: CAB54262.1; GSPDB: GN00023; CESP: H39E23.1b
                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1996
A;Reference number: 218997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Gene: CESP: H39E23.1a; CESP: H39E23.1b
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A;Molecule type: DNA
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A, Cross-references: EMBL:296102; E
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RSSLDNIMKDRWMN 312
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A; Molecule type: DNA
A; Residues: 1-633 <DIE>
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G89287

G89287

Cyprotein H39223.1 [imported] - Caenorhabditis elegans

Cyprotein H39227

Ryanorymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog

A;Title: Genome sequence outlo:99058613; PMID:9851916

A;Note: see websites genome.wusll.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/Cele

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A;Status: preliminary

A;Residues: 1-1246 <STO>

A;Residues: 1-1246 <STO>
A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 99Z (5;Reywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific pro F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #6 F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splide F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splid
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                                                                                                                                                                                                                                IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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A;Gene: H39E23.1
A;Map position: 5
                                                                                                                                                          1 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
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                                                                                        DB 2; Length 1192;
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                                                                                      46.3%; Score 621.5; DB 2;
48.0%; Pred. No. 2.2e-19;
live 52; Mismatches 77;
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RSSLDNIMKDRWMN 422
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                                                                                  Query Match 46.3
Best Local Similarity 48.0
Matches 122; Conservative
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Best Local Similarity
Matches 122; Conserv
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A, Status: preliminary
A, Modecule 1792 - DNA
A, Residues: 1-472 - CDOU>
A, Cross.references: UNIPROT: Q98RL9, GB: AF165818; NID: g13794554; PIDN: AAK39929.1; GSPDB: G.
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A;Title: A yeast gene that is essential for release from glucose repression encodes a pr A;Reference number: A26030, MUID:86289463; PMID:3526554
A;Reference number: A26030
A;Molecule type: DNA A;Residues: 1-633 < CEL.
A;Cross-references: UNIPROT:P06782; EMBL:M13971; NID:g172629; PIDN:AAA35058.1; PID:g1726
R;Dietrich, F.S.
Submitted to the EMBL Data Library, August 1995
A;Describtion: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.
                                                                                                                                   Deng, L.T.; Wu, X.; Rei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cerevi

    yeast (Saccharomyces

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1 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaрв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: AMP-activated protein kinase; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.3%; Score 621; DB 2;
48.0%; Pred. No. 1.2e-19;
tive 52; Mismatches 78
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RITINEIRDHPWFN 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 48.0*
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genome: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: kin(snfl)
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A;Cross-references: UNIPROT:091A88; GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of serine/threonine kinases, fi
                                                                                                                                                                                                                                                                    180 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSD-ACGLIRWLLMVNPTR 238
                                                                                                                                                                                                                                                                                                      60 IIAIHEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NyAlternate names: Qin-induced kinase
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7500
R;Xia, Y: Zhang, Z.; Kruse, U.; Vogt, P.K.; Li, J.
Biochem. Biophys. Res. Commun. 276, 564-570, 2000
A;Title: The new serine-threonine kinase, Qik, is a target of the qin oncoge
A;Reference number: JC750
A;Contents: Embryo fibroblasts
                                                                                                                                                                           120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV
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Best Local Similarity 48.6%
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          239 RATLEDVASHWW 250
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257 RISVPDIRQHQW 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: JC7500
A, Molecule type: mRNA
A, Residues: 1-798 <XIA>
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NyAlternate names: SNP1-related protein kinase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07415
R;Halford, N.G.
submitted to the EMBL Data Library, March 1996
A;Reference number: 216022
A;Accession: T07415
A;Accession: T07415
A;Reference number: 22602
A;Reference number: 22603
A;Reference number: 2
A;Cross-references: EMBL:U33050; NID:g927726; PIDN:AAB64904.1; PID:g927732; GSPDB:GN0006 C;Genetics:
A;Gene: SGD:SNF1; MIPS:YDR477w
A;Cross-references: SGD:S0002885; MIPS:YDR477w
A;Cross-references: SGD:S0002885; MIPS:YDR477w
A;Cross-references: SGD:S0002885; MIPS:YDR477w
A;Description: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Description: Catalyzes the formation of glucose-repressed genes in response to glucose depriv C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Superfamily: AMP-activated protein kinase; protein kinase homology C;Reywords: ATP, autophosphorylation; magnesium; nucleus; phosphoprotein; phosphotransfe F;53-306/Domain: protein kinase ATP-binding motif F;84,103.177,179/Active site: Lys, Glu. Asp, Lys #status predicted F;182,186/Binding site: magnesium (Asn, Asp) Estatus predicted F;182,186/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 YQIVKTLGEGSFGKVKLAYHTTTGQKVALKIINK-KVLAKSDMQGRIEREISYLRLIRHP 113
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al Similarity 48.8%; Pred. No. 1.6e-19;
123; Conservative 45; Міяматсhея я?
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48.2%; Pred. No. 1.7e-19;
tive 57; Mismatches 69
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293 NRISIHEIMQDDW 305
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Best Local Similarity 48.23
Matches 122; Conservative
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Best Local S:
Matches 123,
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                                                                                                                                                                                                                                                                                                                                    205 DIWSLGVVLYVLVCGSLPFDGPNLPTLRQRVLEGRFRIPYFMSEDCETLIRRMLVVDPTK 264
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                                                                         1 YEFLETLGKGTYGKVKKARESSGRL-VAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                       60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRISERDARHFFRQIVSALHYCHQNGI
                                    Gaps
                                    ë,
Length 798;
                                    Indels
46.0%; Score 617.5; DB 2;
48.6%; Pred. No. 2.4e-19;
tive 47; Mismatches 80;
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model Run on:

January 22, 2005, 06:28:10 ; Search time 74.4118 Seconds (without alignments) 1956.274 Million cell updates/sec

US-09-980-464-11\_COPY\_57\_309 1342 1 YEPLETLGKGTYGKVKKARE.....VNPTRRATLEDVASHWWVNW Title: Perfect score: Sequence:

253

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1825181 segs, 575374646 residues Searched:

1825181

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_02:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		Description	Q8cic0 mus musculu	Q9dbv0 m mus muscu	Q80zw3 mus musculu	Q8bzn4 mus musculu	Q9h093 homo sapien	O60285 homo sapien	9	Q6i6d6 mus musculu	Q7qbh4 anopheles g		Q7yu19 drosophila	Aas65135 drosophil	Q9vh05 drosophila	Aaf54517 drosophil	Q8wqg7 caenorhabdi	Q9bibl caenorhabdi	Q96134 homo sapien	Q8cip4 mus musculu	Q8ng37 homo sapien				Q7qbh3 anopheles g	Q96rg0 homo sapien	008679 rattus norv	Q6pdr4 mus musculu	Aah58556 mus muscu	Q15524 homo sapien	homod	Q96hb3 homo sapien	Aah08771 homo sapi
SUMMAKIES		a	QBCICO	Q9DBV0	Q80ZW3	Q8BZN4	ОЭНОЭЗ	ARKS HUMAN	BAA25463	Q616D6	Q7QBH4	Q7KSS0	Q7YU19	AAS65135	Q9VH05	AAF54517	Q8WQG7	Q9BIB1	MRK4_HUMAN	Q8CIP4	Q8NG37	Q804T2	Q9JKE4	Q9JKES	070внз	Q96RG0	008679	Q6PDR4	AAH58556	015524	Q7KZI7	096нвз	AAH08771
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de		Match	100.0		99.0	99.0	96.3	84.1	84.1	76.4		•	61.3	61.3		61.3		•	49.6		•	•		•	•	•	٠	48.2	48.2		48.2	٠	48.2
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Q8vhf0 rattus norv	Q8br95 mus musculu	P92958 arabidopsis		Q802w0 brachydanio	Q6int7 xenopus lae	Aah72186 xenopus l	O08678 rattue norv		Q7zyl7 xenopus lae		cucumia	075271 homo sapien	Q6v8y5 physcomitre
QBVHF0	Q8BR95	P92958	P92968	Q802W0	OGINT7	AAH72186	008678	QBVHJS	Q7ZYL7	QBQGV3	P93113	075271	Q6V8Y5
7	~	~	~	~	~	~	~	7	~	7	~	~	7
797	888	512	512	722	792	792	793	795	176	785	504	462	542
 48.2	48.2	48.0	48.0	48.0	47.9	47.9	47.9	47.9	47.8	47.8	47.8	47.7	47.7
647.5	647.5	644	644	643.5	642.5	642.5	642.5	642.5	641.5	641.5	641	640.5	640.5
32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200013B22 product:weakly similar to PROBABLE SERINE/THREONINE-
PROTEIN KINARS KIAROS37 (EC 2.7.1..) (Mus musculus adult male cecum
CDNA, RIKEN full-length enriched library, clone:9130215K18
product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                             1 YEPLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
                                                                                                                                                                                                                                                                                                        Gaps
              InterPro; IPR000719; Prot kīnase.
InterPro; IPR00230; Ser thr pkinase.
InterPro; IPR00230; Ser thr pkinase.
InterPro; IPR00230; Ser thr pkinase.
From Pr00069; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
SWART; SN0020; STKc; I.
PROSITE; PS00101; PROTEIN KINASE ATP; I.
PROSITE; PS00101; PROTEIN KINASE DOM; I.
ATP-binding; Kinase; Serine(hreonine-protein kinase; Transferase.
SEQUENCE 631 AA; 69745 MW; C6C9042247D9174F CRC64;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                              100.0%; Score 1342; DB 2; Length 631; 100.0%; Pred. No. 1.2e-97;
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTium;
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STRAIN=C57BL/6J; TISSUE=Cecum, and Lung;
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IPR011009; Kinase like
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253; Conserv
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InterPro;
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Q9DBV0
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the RIERY Gromen Exploration Research Group Phase 1 & 11 Tean;

"Nalyagia of the mouse transcriptome based on functional annotation of
a 0,770 fail-length CDRAs."

Nature 440:563-573 (2002).

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg E., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg E., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zoordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Toochiyuki S., Carninci P., Prange C.,
Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodecgren B.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakeeley R.W., Tucchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                             57 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI 116
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                                                                                                                                                                                                                                             Gaps
SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_DAF; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 631 AA; 69806 MW; D51C042DE6CC174B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
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STRAIN=C57BL/6; TISSUE=Brain;
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STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
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                                                                                                                                                                                                              al Similarity 100.
253; Conservative
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Name=1200013B22Rik;
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117 IAIHEVGRSRLVTVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALH
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                 HSSP, P31751; 1GZK.

MGD; MGI:1921387; 1C20013B22Rik.

MGD; MGI:1921387; 1200013B22Rik.

GO; GO:0004674; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR002291; Ser_thr_pkinase.

InterPro; IPR008271; Ser_thr_pkinase.
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01-MAR-2004 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus mustalus adult male diencephalon cDNA, RIKEN full-length
library, clone:9330154N24 product:weakly similar to PROBABLE
SERINE/THEREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-).
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; BCO46833; AAH46833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.0%; Score 1328; DB 2; Length 639; 96.9%; Pred. No. 1.6e-96;
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STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=99279253; Pubmed=10349636;
Carinci P., Hayashizaki Y.;
Carinci P., Hayashizaki Y.;
Meth-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Diencephalon;
MEDLINE=21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 96.9
Matches 253; Conservative
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A FANDAN-ECSPBL/65; TISSUE-Diencephalon;
A FANDAN-ECSPBL/65; TISSUE-Diencephalon;
A FANDAN-ECSPBL/65; TISSUE-Diencephalon;
A FANDAN-ECSPBL/65; TASAWA K., ARIMDIA T., ARABAIZUME W.,
A HAYSCHOW W., Hirancho K., Hiracka T., Hirozane T.,
A Katch H., Kawai J., Kojima Y., Kondo S., Komno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saico R., Saicoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AKOJ4082; BAC28575.1; -.
                                                                                                                                     the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                              STRAIN=CS7BL/6J; TISSUE=Diencephalon; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/60; TISSUE=Diencephalon; STRAIN=C57BL/60; TISSUE=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Incure K., Tione Y., Kira A., Hayashizaki Y., Rurani Integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ET; 1.
ATP-binding; Kinase; Serine/threonine-protein Kinase; Transferase.
SEQUENCE 639 AA; 70632 MW; FB98
                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:1921387; 1200013B22Rik.
GO:0005524; F:ATP binding; IEA.
GO:0004674; F:protein serine/threonine kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:001640; Fitransferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
Probom; PD000001; Prot kinase; 1.
Probom; PD000001; Prot kinase; 1.
Probom; PD000001; Prot kinase; 1.
                                                                             SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Diencephalon;
The FANTOM Consortium,
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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ATP-binding;
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MEDINEE-199825;

WEDINEE-199825;

WEDINEE-208825;

WEDINEE-208825;

WEDINEE-208825;

WEDINEE-208825;

WALE STREEL WITH GROWN COLOUR STREET C.E., Sheller G.D.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marushna K., Farmer A.A., Rubin G.M., Hong L.,

And Diatchenko L., Marushna K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Raha S.S., Loquellano M.A., Peres G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Wilalon D.K., Muzny D.W., Sodergen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Mitting M., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Warra M.A.,

A Jones S.J., Marra M.A.,

A Generation and initial analysis of more than 15,000 full-length human
                      57 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI 116
                                                                                                  296
                                                                                                                                                        113 YCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGK 1,72
9
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                                                                                                                                                                               IAIHE------VFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALH
  1 YEFLETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHI
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SEQUENCE FROM N.A.
Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OGT-2004 (TrEMBLrel. 16, Last sequence update)
01-OGT-2004 (TrEMBLrel. 28, Last amontation update)
Hypothetical protein DKPZp434J037 (Hypothetical protein SNARK)
(Hypothetical protein FLJ90349).
Name=DKFZp434J037, Synonyms=SNARK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Testis;
Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          628 AA.
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Gaps

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Indels

0; Mismatches

Query Match
Best Local Similarity 96.9%;
Matches 253; Conservative

Score 1328; DB 2; Length 639; Pred. No. 1.6e-96;

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code for large proteins in vitro.

DNA Res. 5:31239(1998).
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                                                                                                                                                                                                                                                                                                  starvation.
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Best Local Simi
Matches 209;
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Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. IX.
Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K., Masuho Y., Ono T., Okano K., Yoshikawa Y., Actsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K., Sasaki N., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. EMBL; BC017306; AAH1706.1; -.
EMBL; BC017306; AAH1706.1; -.
EMBL; AK074830; BAC11234.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                         GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016768; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00279; Ser_thr.pkinase.
InterPro; IPR00279; Ser_thr.pkinase.
InterPro; IPR008271; Ser_thr.pkinase.
France Pro; IPR008271; Ser_thr.pkinase.
France Pro; IPR0069; Pinase; InterPro; Pin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.3%; Score 1293; DB 2; Length 6
95.7%; Pred. No. 9.3e-94;
ive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000001; Prot Kinase; 1.
SMART; SM00220; S TKC; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-brading; Hypothetical protein; Kinase; Serine/throonine-protein Kinase; Transferase.
SEQUENCE 628 AA; 69611 WW; F76FBBIBF94F4C87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
AMPR-related protein kinase 5 (EC 2.7.1.37).
Name-ARKS; Synonyms=KIAA0537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   661 AA
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060285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 IISIYEVFENKDKIVIIMEYASKGELYDYISERRRLSERETRHFFRQIVSAVHYCHKONGV 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
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                                                                                                                                                                             Suzuki A., Kusakai G.-I., Kishimoto A., Lu J., Ógura T., Lavin M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: Expressed at high levels in heart and brain, and at lower levels in skeletal muscle, kidney, ovary, placenta, lung and liver.
SIMILARITY: Belongs to the Ser/Thr protein kinase family.
new cDNA clones from brain which can :ro.";
                                                                                                                                                                                                                                "Identification of a novel protein kinase mediating Akt survival signaling to the ATM protein.";
J. Biol. Chem. 278:48-53(2003).
-!- FUNCTION: Involved in tolerance to glucose starvation.
Phosphorylates ATM.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- ENZYME REGULATION: Activated by PKB/AKT1 during glucose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                            CHARACTERIZATION, AND MUTAGENESIS OF SER-600.
MEDLINE=22393479; PubMed=12409306; DOI=10.1074/jbc.M206025200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
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806F37D52CA4718F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.1%; Score 1128.5; DE ilarity 82.3%; Pred. No. 1e-80; Conservative 24; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000719; Prot Kinase.
Interpro; IPR00071; Ser thr_pkin_AS.
Prodom; PD00069; Pkinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Phosphorylatjon; Polymorphism.
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61 YISERRRISERETRHFFRQIVSAVHYCHRNGVVHRDLKLENILLDDNCNIKIADFGLSNL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene: III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous cDNAs Identified by Screening of Terminal Sequences of cDNA Clones Randomly Sampled from Size-fractionated Libraries.";
DNA Res. 10:167-180(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 IKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVPENSSKIVIVMEYASRGDLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 YISERPRISERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADFGLSNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probom, PD000001; Prot Kinase; 1.
SWART; SM00220; S_TKC; 1.
SWART; SM00219; TyrKC; 1.
PROSTE; PS500101; PROTEIN KINASE DOW; 1.
PROSTE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
-!- GAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AAABO1008879; EAABO421.1; -.
GO, GO:0005524; F:ATP binding; IEA.
GO, GO:0005547; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
                                                                                                                                                                                                                            Okazaki N., Kikuno R., Nagase T., Ohara O., Koga H.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB182364; BAD23995.1; --
InterPro; IPR011099; Kinase like.
InterPro; IPR002719; Prot Kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR004271; Ser thr pkinase.
InterPro; IPR004271; Ser thr pkinase.
Pro0069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.4%; Score 1025; DB 2; Length 575; 82.3%; Pred. No. 1.3e-72; cive 23; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 KQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASHWWVNW 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575 AA; 64949 MW; 3CA0796FB4199D2B CRC64;
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 5:31-39(1998).
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Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Hagase T., Ohara O., Koga H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi; ; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.1%; Score 1128.5; DB 2; Length
82.3%; Pred. No. 1.1e-80;
ive 24; Mismatches 20; Indels
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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ATIEDIANHWWVNW 345
          ||:||:||:||
| ATIEDIANHWWVNW 308
                                                                                                                                                                                                                                                                                                                                                                     KIAA0537 protein (Fragment)
KIAA0537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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nes 209; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Brain;
                                                                                                                                                                                                                                             BAA25463;
02-mar-2004
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SEQUENCE
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                                           295
                                                                                                                                                                                                           BAA25463
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BAA25463

BAA25463

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CO C BUK
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FLYBASE;
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     MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
An K.H., Doyle C., Baxern E.G., Helt G., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Besson K.Y., Benoes P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davis S. P.,
A de Pablos B., Delcher A., Deng Z., Mays R.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Durbin K.J., Evangeliste C.C., Ferraz C., Ferriera S., Fleischmann W.,
R. Fosler C., Gabriellan A.E., Garg N.S., Glabatt W.M., Glasser K.,
All Harvis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                 60 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 119
                                                                                                                                                                                                                                                                                120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                                                                                                                                                                                                                     164 CHRDLKLENILLDEHGNAKIADFGLSNVFDEQRLLATFCGSPLYASPEIVKGTPYQGPEV 223
                                                                                                                                                                                                                                                                                                                                                                        DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR 239
                                                                                                                                                                                                                                                                                                                                                                                         224 DCWSLGVLLYTLVYGAMPFDGANFKRLVKQISQGDYFEPKKPSRASPLIREMLTVCPSHR 283
                                                                                                                                                                                                                   1 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 59
                                                                                                                                                                                            Gaps
                                  Pfam; PF00069; PKinase; I. ProDom; PD000001; Proc kinase; I. PROSITE; PS001001; PROTEIN KINASE ATP; I. PROSITE; PS00110; PROTEIN KINASE DOM; I. PROSITE; PS00108; PROTEIN KINASE DOM; I. ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                           1;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                  DB 2; Length 383;
GO:0006468; P:protein amino acid phosphorylation; IEA
                                                                                                                                                                61.4%; Score 824.5; DB 2; Length 61.3%; Pred. No. 6.1e-57; ive 44; Mismatches 53; Indels
                                                                                                                                        383 AA; 43133 MW; 294732D45CFC1023 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1180 AA
          InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
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284 ANIEQICNHWWVN 296
                                                                                                                                                                            Best Local Similarity 61.33
Matches 155; Conservative
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05-JUL-2004 (TrEMBLrel.
CG11870-PD.
ORFNames=CG11870;
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Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalubh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
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Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spralling A.C., Staplecon M., Strong R., Sun B.,
Syirskas R., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Moodagef W., Zhon G., Zhao Q., Zhan M., Zhang G., Zhao Q., Zheng L.,
Cheng X.H., Zhong F.N., Zhong W., Zhao G., Zhao G.,
The genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frige E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halpern A., Calniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Calniker S.E., Moams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutron G.G., Venter C. Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.; Pfnishing a whole-genome shotgun: release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lewis S.E.; "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AE003686; AAS65135.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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InterPro; IPR000719; Prot kinase.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008290; Sar Lhr pkinase.
InterPro; IPR008271; Sar Lhr pkin AS.
InterPro; IPR001245; Tyr pkinase.
ProDom; PD00069; Pkinase; I.
SWART; SM00220; STKC; I.
SMART; SM00219; TyrKC; I.
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310 ASIEQICSHWWVN 322
                                                                                                                                                                                                                                                                                     240 ATLEDVASHWWVN 252
          Query Match
Best Local Similarity 61.74
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                   120 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 179
                                                                                                                                       5
                                                                                                                                                                                                                                                                       CHRDLKLENILLDEKGNAKIADFGLSNVFDDQRLLGTFCGSPLYASPEIVEGTPYQGPEV
                                                                                                                                       1 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH
                                                                                                                                                                                                                                                                                                       DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRR
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1. SURLLAREAY: Belongs to the Ser/Thr protein kinase family.

BMBL; BT010033; AAQ22502.1; -.

R PlyBase; PESH00031940; CG11870.

R GO; GO:0006524; F:ATP binding; LEA.

GO; GO:000674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

INTERPO; IPR000219; Prot kinase.

R InterPro; IPR0002209; Ser thr pkinase.

R InterPro; IPR000209; Ser thr pkinase.

R RPDOGN; PR000001; Prot kinase; 1.

R RWART; SM00220; S TK0; 1.

R ROSITE; PS00107; PROTEIN KINASE ATP; 1.

R ROSITE; PS00107; PROTEIN KINASE DGM; 1.

R RPOSITE; PS00108; PROTEIN KINASE DGM; 1.

R RP-Dinding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 1180 AA; 127684 MW; 2CD790A4F3DBCSOC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B., Goorge K., Gonzallez M., Gaurin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S. Partel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threomine-protein kinase; Transferase.
SEQUENCE 1180 AA; 127743 MW; A88A012664046EC6 CRC64;
                                                                                                           ij
                                                                             61.3%; Score 822.5; DB 2; Length 1180; 61.7%; Pred. No. 3.3e-56; Indels 1; ive 44; Mismatches 52; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                                                                           310 ASIEQICSHWWVN 322
                                                                                                              Conservative
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                                                                                 Query Match
Best Local Similarity
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Celniker S.;
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REAL MEDILINE STORONGS, PubMed=10731132;

RADELINE FOOM N.B.

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RADELINE STORN R.B.

RADELINE STORN R.B.

RADELINE STORN R.B.

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RADELINE R.C., Rogers Y.H., Blazej R.G., Chenge M., Henderson S.N.,

RADELINE R.C., Rogers Y.H., Blazej R.G., Chenge M., Pfeiffer B.D.,

RADELINE R.B.

RADELINE C., Rogers Y.H., Blazej R.G., Chenge M., Pfeiffer B.D.,

RADELINE R.M. Basu A., Baxedale J., Bayraktaroglu L., Beasley E.M.,

RADELINE R.M., Cawley S., Burler H., Cadieu E., Center A., Chandra I.,

RADELINE R.D.

RADELINE R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADELINE R.D.

RADELINE R.C., Revangelista C.C., Ferraz C., Ferriera S., Fleistchmann W.,

RADELINE R.R.

ROGIER C., Gabrielian A.E., Gargn N.S., Gelbart W.M., Glasser K.,

RADELINE R.R.

ROGIER C., Gabriellan A.E., Garrell J.H., Gu Z., Guan P., Harris M.,

RADELINE R.R.

RADELINE R
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Last annotation update)
    DB 2;
61.3%; Score 822.5; DB 2
61.7%; Pred. No. 3.3e-56;
iive 44; Mismatches 52
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10 FDIIKKLGQGTYGKVQLGINKETGQEVAIKTIKKCKIEAEADLVRIRREVQIMSSVHHPN 129
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Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao D., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a Whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lewis S.E.; ^{\prime} "Annotation of the Drosophila melanogaster euchromatic genome: a
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SEQUENCE 1180 AA; 127743 MW; A88A012664046EC6 CRC64;
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Matches 156; Conservative
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REMINES_CROWN N.A.

REMAILINES_CO196006; Pubmed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocavne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocavne J.D.,

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Radion R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballaw R.M., Bavu A., Baxendala J., Bayraktarolu L., Beasley E.M.,

RA Beeson K.Y. Bence P.V., Berman B.P., Bhandari D., Blothakov S.,

RA Buttis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chenfra I.,

RA Buttis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,

RA Buttis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dagan-Rocha S., Dunkov B.C.,

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RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,

Alalahi M., Kalush F., Karpen G.H., Kez., Kenniand D. Laiz Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Alak R. Molton K.A., Molton M., Mobarry C., Morris J., Moshrefi A.,

Rollon B.E., Kodira C.D., Kraff C., Kravitz S., Kulp D., Laiz Z.,

Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

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Rollon D.R., Nolson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

Rancel S., Siden-Kiamos I. S., Ronson D.,

Reinert K., Remington K., Saunders R., Venter E., Wang X.,

Reinert K., Zeveri J.S., Zhan M., Zhong W., Zhon Y., Zhong W., Zhon Y., Zhong W., Zhon W., Zhong W., Zhon W., Zhong W., Zhon W., Shuba R., Wallsass S.M., Woodager, Woller E., Wallsesen B., Zhon M., Schene S., Zhon K., Schene S., Schene S., Schene S., Schene S., Schene S., Schene S., 
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MEDLINE=22446065; PubMed=12537568;
MEDLINE=22446065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patcher B.D., Frichards S., Sodergren E.J., Svirskas R., Tabor P.E., Man K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoā; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_Tax1D=7227;
                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                PRT; 1427 AA.
                                                                                                                                                                                                            Created)
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                             310 ASIEOICSHWWVN 322
240 ATLEDVASHWWVN 252
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                             MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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ProDom, PRO00001; Proc Kinase; 1.
SMART; SM00220; STKC; 1.
SMART; SM00210; TYRK; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS00109; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 1427 AA; 153443 MW; 530928D0A057BSC8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; ASR03686; AAF54517.3; -.
INFSP; Q63450; IA6.
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                                                                                                                                                                                           a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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hes 156; Conservative
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RX PENGUNCE KYMEN N.A.

RX MEDLINE-20196006; PubMed=10731132;

RA dammatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA damnatides P.G., Scherer S.E., In P.W., Hoskins R.A., Galle R.F.,

RA denorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,

RA Ballew R.M., Bane M., Barandale J., Bayraktaroglu L., Beasley E.M.,

Benchon R.C., Bouck D., Burnen B.P., Bhandari D., Bolahakov S.,

RA Borkova D., Botchan M.R., Buller H., Cadieu B., Center A., Chandra I.,

RA Buris K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,

RA Buris K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,

RA Buris K.C., Busam D.A., Buller H., Cadieu B., Dow I., Dietz S.M.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Buris K.C., Busam D.A., Buller H., Cadieu B., Center A., Chandra I.,

RA Buris K.J., Evangelista C.C., Ferraz C., Ferriara S., Plaikov B.C., Dunn P.,

RA Haris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J.,

RA Haris N.L., Havey D., Heiman T.J., Hermandez J.R., Houck J.,

RA Jalai M., Kalush F., Karpen G.H., Kaz Y., Kanison J.A., Ketchum K.A.,

Jalai M., Kalush F., Karpen G.H., Kraft C., Kravitz S., Kulp D., Lai Z.,

Liu X., Mattei B., McIntoon T.C., Morris J., Mochecon D.,

RA Mount S.M., Moy M., Murphy E., Murphy L., Murzhy D.M., Nelson D.L.,

Ra Bazzolo M., Pitchama G.S., Pan S., Pollard J., Morley K.D.,

RA Reinert K., Remington K.A., Nixon K., Wonter E., Wang A., Wang X.,

Randers R., Jeckel Kamao I., Simpson M., Stupski M.P., Smith T.,

Randers R., Jeckel J., Worley K.C., Wu D., Yang S., Yao Q.,

RA Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.,

RA Williams S.M., Woodager, Wolly M., Welley R., Zhou S., Zhu S., Z
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MEDLINE=2242605; PubMed=12537568;

MEDLINE=2242605; PubMed=12537568;

Rati S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

Ratel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacieb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

"Finishing a Whole-genome shotgun: release 3 of the Drosophila

melanogaster euchromatic genome sequence.",

Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                     01-APR-2004 (TrEMBLrel. 27, Created)
01-APR-2004 (TrEMBLrel. 27, Last sequence update)
01-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                         1427 AA
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310 ASIEQICSHWWVN 322
                                                                                                                                    PRELIMINARY;
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SEQUENCE FROM N.A.
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240 ATLEDVASHWWVN 252

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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
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                                      Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stappeton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
Hypotherical protein B0496.3.
Caenorhabditis elegans.
Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome: a systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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FlyBase; FBgn0037804; CG11870.
SEQUENCE 1427 AA; 153444 MW; 530928D0A057B5C8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
MEDLINE=22426069; PubMed=12537572;
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310 ASIEQICSHWWVN 322
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Best Local Similarity 61.7<sup>3</sup>
Matches 156, Conservative
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R GO, GO.0004674; F.ATP binding; IEA.

R GO; GO.0004674; F.PDTOLEIN BERING/threonine kinase activity; IEA.

R GO; GO.0004674; F.PDTOLEIN BERING/threonine kinase activity; IEA.

R GO; GO:0004674; F.PDTOLEIN amino acid phosphorylation; IEA.

R GO; GO:0004674; F.PDTOLEIN amino acid phosphorylation; IEA.

R INTERPRO; IPR001009; GOW_HINGSE INC.

R INTERPRO; IPR00019; Prot Kinase.

R INTERPRO; IPR000871; Ser_thr_pkin_AS.

R Ffam; PF00069; PR000001; Prot Kinase; 1.

R PROSITE; PS001007; PROTEIN KINASE ATP; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R PROSITE; PS00109; PROTEIN KINASE; 7; 1.

KW ATP-binding; HYPOCHELICAI protein; Kinase;

SEQUENCE 1566 AA; 178267 MW; 1E540608AF08059A CRC64;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Murray J., Le T.T.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
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ilarity 61.7%; Pred. No. 2.3e-55;
Conservative 33; Mismatches 63;
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Matches 156; Conserv
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January 24, 2005, 11:04:39; Search time 5813.23 Seconds (without alignments) 11866.113 Million cell updates/sec
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## ALIGNMENTS

RESULT 1 AKO04737 LOCUS DEFINITION VERSION VER	AKO04737  Mus musculus adult male lung CDNA, RIKEN full-length enriched library, clone:1200013B22 product:weakly similar to PROBABLE SERINGTHREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1) [Homo AKO04737.  AKO04737.  AKO04737.  AKO04737.  AKO04737.  GI:26334437  HTC; CAP trapper.  Mus musculus (house mouse)  10 and Hayashizaki,Y.  Garninci,P. and Hayashizaki,Y.  Meth. Enzymol. 303, 19-44 (1999)  99279253  10349636  2 carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  Normalization and subtraction of cap-trapper.selected CDNAs to prepare full-length CDNA libraries for rapid discovery of new genes Genese Eull-length CDNA libraries for rapid discovery of new genese 20499374
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KHHHKHVERHRYEPLETIGKGTYGKTYGKKARRSSGRUVALKSTRKDEVLLHTR
REIELMSLAHPHIALHEVERENSKUVINGYASRUDLYDYISERPRLSERDARHF
RQIVSALHYCHQMGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPL
YASPEIVKRYKRYVGPRVDSWSLSVLLYILYHCHWPPDGQDPRTLYLKQISENGAYFEPPK
PSDACGLIRMLLMYMPTRAFLEDVASHWWYNWGYTTGVGEGERLEGGHPSGPPGRA
SMADWLRRSSRPLLENGAKVCSFFKQHVPGGGSTVPGLBRQHSLKKSRKENDMAQNLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product; putative weakly similar PROPEIN KINASE WEAKLY SIMILAR. PROTEIN KINASE KRAAOS37 (EC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285, evidence: FASIY, 56.0%ID, 98.6%length, match=1849)"
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PRKGILKKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGI
LKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARPSRPSGAVSEDSILSSESFDQLDL
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/tissue type="lung"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev kiage="adult"
94. _1989
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On Dec 10, 2002 this sequence version replaced gi:12836134.
Please visit our web site (http://genome.gsc.riken.jp/) for further
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                                 Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2899)
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FANTOM Consortium and the RIKEN Genome Exploration Research
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/db_xref="GI:12836135"
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AK033672 AK033672.1 GI HTC; CAP trapp Mus musculus () Musc	Normalization prepare full-1 Genome Res 10 20499374 11042159 3 Shibata,K., It Konno,H., Akiy, Sumi,N., Ishii Yamamoto,R., M Fujiwake,S., II Yonedan,Y., Ish	RIKEN integration of genome Res. 10 20530913 11076861 4 4 The RIKEN Genome Fantom Consort Functional ann Nature 409, 68 5 The FANTOM Congroup Phase I Analysis of the Analysis of the Nature 420. 56 6111 Nature 420. 56	Adachi, J., Aiz, Hydachi, J., Aiz, Hydashida, K., Hori, F., Imota, Katoh, H., Kawa Koya, S., Kawa Koya, S., Sa Okazaki, Y., Sa Sano, H., Sasak Sogabe, Y., Tan Muramateu, M. a Direct Submiss Submitted (16-) Physical and C Exploration Re RIKEN Yokohama Kanagawa 230-0 URL: http://gen
ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE JOURNAL
961 CTGCGTGAGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTA 1020	1201 TCTCGCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAGTCCTCT   1260	1381   CAGCGTGAATCTGGTTACTACTCCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGAC	1621   GCCGGCCCGGCCCCTCAGGGGCTGTGAGTGAGGACATCCTGTCCTCCCGGGTCC
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AK033672

3098 bp mRNA linear HTC 03-APR-2004 Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130215K18 product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-) [Homo sapiens], full insert sequence.

RESULT 2 AK033672 LOCUS DEFINITION

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Libert Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suchiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegue.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-922, Fax:81-45-503-9216)

Exx:81-45-503-9216)

Exx:81-45-503-9216

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.jp/
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TCCAACCTGTACCACAAAGGCAAGTTCCTCCCAGACGTTCTGTGGGGAGCCCTCTCTACGCC
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     CTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAGCGGGGACGCCAGGCATTTCTTC
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                                                                                                                     AAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTC
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Wanagawa 230-0045, Japan (E-mail:genome-res@gec.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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The FANTOM Consortium and the RIKEN Genome Exploration Research
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
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2869 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male diencephalon cDNA, RIKEN FUIL-length
enriched library, clone:9330154N24 product:weakly similar to
PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-)
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Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
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                              Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submitted (16-0VO-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Pred. No. 0;
0; Mismatches 120;
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
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/db_xref="taxon:10090"
<1._.>1896
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      d. No. 2.1e-236;
Mismatches 722;
      Pred.
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    60.08;
   Best Local Similarity 60.0
Matches 1116; Conservative
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11 (bases 1 to 1887)
12 (d. M. A., Ganowski, S., Nielson, R., Thomas, P., Kejariwal, A., Fodd, M. A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
                                            CACAGGCTTCAGGGCTCCTCCTCCACGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT
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/clone="IMMASE:9718428"
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/clone lib="NIH BMAP FD0"
/clone lib="NIH BMAP FD0"
/clone lib="NIH BMAP FD0"
/clone lib="INH BMAP FD0"
/clone lib="INH BMAP FD0"
/clone lib="Inh library was constructed according to Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNB was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EOR I adaptor, digested with Not I, and then cloned directionally into pYx-Msc vector. The library tag sequence located between the Not I site and the polyh tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Amatony Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
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Tissue Procurement: Dr. James Lin, Univeristy of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                   This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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Pred. No. 2.8e-167;
0; Mismatches 5;
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1. .726
/organism="Mus musculus"
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/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:5718428"
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Best Local Similarity 98.8%;
Matches 720; Conservative
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     GCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACCCCTGGCCCTGGAGCGCCAGC 1114
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NH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                            ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG
                                                                                                                  ATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAGTCTCTCCACACAGAGACACGG
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MushamC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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0
                                                                               Length
Institute of Mental Health (NIMH)."
                                                                         Score 672; DB 7;
Pred. No. 3e-164;
                                                                      35.5%; Score 672; DB
ilarity 100.0%; Pred. No. 3e-
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                           1338
                                                                                                                                                                                                                          1399 TACTCCTCCAGAGCCCAGGGGAGTCTGGGGAACTCTTAGACGCCAGTGATGTGTTTGTG 1458
                                                                                                                                                                                                                                                                                                                                    AGTGGGGACCCCGTGGAGCCAGAAGTCTCCACAGGCTTCAGGGCTCCTCCTCCACCGCAAG 1518
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                                                                            540
                                                                                                                                                                 541 GTATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACACGTGAATCTGGTTAC 600
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Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Parrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Location/Qualifiers
                                                                                                                                                                                                                                                                                TACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATGTGTTTGTG 660
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 672)
                                                      1. .672
/organism="Mus musculus"
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/strain="C57BL/6"
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Mus musculus
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CO424322
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1534 AATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCTG
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BG174288.1 GI:12680991
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/clone="Indexon:10090"
/tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="Bub10B (TI phage resistant)"
/lab_host="Bub10B (TI phage resistant)"
/clone lib="NIH BMAP_GIO"
/clone lib="NIH BMAP_GIO"
/clone="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/clone="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/clone="Organ: Brain; Vector: pYX- Asc; Site_1: BcoR I;
/clone lib="NIH BMAP_GIO"
/clone lib="NIH BMAP_GIO"
/clone lib="NIH BMAP_GIO"
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/clone lib="NIH BMAP asc; Site_1: BcoR I;
/clone lib="NIH BMAP asc; Site_1: BcoR I;
/clone lib="NIH Agarcas"
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/clone Brain Anatomy Project (BMAP): 'Gene Discovery in the
/clone library library was created for the University
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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                                                                                                                                                                                                                                                                                                                                      1. .655
/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6"
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FV9E\"
/strain="FV9E\"
/strain="FV9E\"
/db xref="taxon:10090"
/clone="INAGE:4457398"
/tissue type="tumor, biopsy sample"
/dev stage="3 months, virgin"
/dev stage="3 months, virgin"
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/clone=lib="NCI_CGAP_Mam1"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
/note="Torgan: mammary; Vector: pCMV-SPORT6; SalI;
/note="Torgan: mammary; Vector: pCMV-SPORT6; SalI;
/note="Torgan: mammary; Vector: pCMV-SPORT6; SalI;
/note="Torgan: mammary; 
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602334589FI NCL_CGAP_Mam1 Mus musculus CDNA clone IMAGE:4457398 5',
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
I (Dases 1 to 805)
II (Dases 1 to 805)
INH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                              481 AATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTAACACCCTAGCACCTTTGGCTCCCTG
                                                                                                                                                                                                GACCAACTGGCCTCCTCCCATCCTGCAGCCCGGCCCAGCCGCCCCTCAGGGGCTGTGAGT
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life I.M.A.G.E. Consortium
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can http://image.lln.gov
Flound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10254 row: b column: 23
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100.0%; Pred. No. 1.9e-157;
tive 0; Mismatches 0;
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Matches 646; Conservative
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NISC_iv09h10.w1 Soares NMBP2 pituitary Mus musculus cDNA clone
IMAGE:4317546 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 646)
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Clone distribution: NCI-CGAP clone distribution information can }
found through the I.M.A.G.E. Consortium/LLNL at:
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                   GGCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTTCTACGCCTCGCCTGAGATAGTCAAC
                                                                                                                                                                                                           GGGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCCTGTACATC
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: W. Bento Soares Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
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MGI:1598314
Plate: LLAM9921 row: O column: 19
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Location/Qualifiers
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Location/Qualifiers
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/strain="C57BL/6"
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CA319312.1 GI:24537436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db xref="taxon:10090"
/clone="IMAGE:4223267"
/lab_host="DH10B (T1 phage-resistant)"
/clone lib="NUI CGAP kid14"
/note="Organ: kidney" Vector: pCMV-SPORT6; Site_1: NotI;
/note="Taxon: Note with the constructed by Life and the constructed by Life Technologies. Note: this is a NCI_CGAP Library. |
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                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 948)
HH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAM9811 row, g column: 12
High quality sequence stop: 651.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="FVB/N"
                                                                  musculus (house mouse)
                                 BF789245.1 GI:12094281
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Mus musculus
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/bricain="colubro"
/db_xref="taxcon:10000"
/clone="IMAGE:6816569"
/clone="WadE:6816569"
/dev_stage="whole brain"
/dev_stage="whole brain"
/dev_stage="mbryo 13.5,14.5,16.5,17.5dpc"
/lab_host="PH10B (TI phage resistant)"
/clone lib="NIH BMAP FW0"
/clone lib="NIH CON"
/clone lib="NIH Lib="NIH"
/clone lib
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Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musculus

I (bases 1 to 795)

National Institutes of Health, Mammalian Gene Collection (MGC)

AL (hopublished (1999)

Contact: Robert Strausberg, Ph. D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://mage.lln.gov
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1347 GCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTC
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/mol_type="mmxna"
/db_xref="taxon:960"
/tissue_type="embryonic stem cells, embryoid bodies
derived_from H1, H7 and H9 cells"
/clone_libe="GRN EB"
/note="oligo dT primed, full-length enriched cDNA library
from embryoid body outgrowths derived from hES cell lines
H1 (p22), H7 (p29), and H9 (p26) maintained in feeder-free
conditions."
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              Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, 1
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 782 Std Error: 0.00.
                                                                                                                                                                                                                                                                                                                                  Score 627.6; DB 7;
Pred. No. 1.3e-152;
0; Mismatches 89;
                                                                                                                              1. .782
/organism="Homo sapiens"
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Best Local Similarity 88.5%;
Matches 692; Conservative 0
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                                                  25;
                     Length 795;
                                                Indels
                 Score 640; DB 6; I
Pred. No. 7.3e-156;
); Mismatches 0;
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ilarity 96.5%;
Conservative
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                Query Match
Best Local S:
Matches 685
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CN261003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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ï 210

Gaps 1;

Length 782; Indels 330

270

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240

450

300

510

360

570

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690
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GGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTC 630
                              421 GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG 480
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                                                            631 CAGACGTTCTGTGGGAGCCCTCTCTACGCCTGGCCTGAGATAGTCAACGGGAAGCCCTAT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

 (bases 1 to 782)

17000424711689 GRN\_EB Homo CN261003

CN261003.1 GI:47277417

sapiens (human) sapiens

Homo Homo

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that control human Es cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)

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Search completed: January 24, 2005, 20:17:48
Job time : 5819.23 secs
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// Ab xref="taxon:9606"
// Clone="INAGES:796791"
// Lissue type="lymphona, cell line"
// Lisue type="lymp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases I to 1069)

NIH-MOC http://moc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt cDNA Library Preparation: Rubin Laboratory Pont Sequencing by: Agencourt Bioscience Corporation Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Fligh quality sequence stop: 775.

Location/Qualifiers

Location/Qualifiers
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_6704953 NIH_MGC_99 Homo mapiens cDNA clone IMAGE:5796791
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                                           721 GAACCCCACCCGCCGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGG 780
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Pred. No. 3e-149;
0; Mismatches 122; Indels
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Best Local Similarity 84.9%;
Matches 721; Conservative
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                                                                                                                391 Aagarcigargcacaracggaggaggarrgagarcargrcarcacracaccaccrcaca
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APPLICANT: Bird, Timothy A.
APPLICANT: Wirca, G. Duke
APPLICANT: Wirca, G. Duke
APPLICANT: Martin, Unja
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KIN
FILE REFERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/10/355,975
CURRENT FILING DATE: 2003-01-30
PRIOR PRILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
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Publication No. US20030162277A1
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Sequence 87, Appl
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2: \cgn2_6/ptodata/2/pubpna/PCT_MEW_PUB.seq:*
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Result

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Sequence 3, Appli Sequence 5, Appli Sequence 1, Appli Sequence 81, Appl Sequence 1541, Ap Sequence 1541, Ap

Sequence 6703, Sequence 37, 7 Sequence 36, 7 Sequence 94, 7

Sequence 34, P Sequence 10, P Sequence 14, P Sequence 9, Ap

Sequence 32, Sequence 92, Sequence 97, Sequence 33,

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PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin version 3.0
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PUBLICATION NO. US20040132025A1
GENERAL INFORMATION:
APPLICANT: BRUCKER, Daniel J.
APPLICANT: BROSEN, Cheryl F.
APPLICANT: LEFEBVRE, Diana L.
TILLE OF INVENTION: AMPRERELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REPERENCE: DPA-DRUCZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514
CURRENT APPLICATION NUMBER: US/10/343,514
FRIOR APPLICATION NUMBER: PCT/CA01/01109
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/222,650
PRIOR PRIOR APPLICATION NUMBER: US 60/224,613
PRIOR PRIOR DATE: 2001-03-12
PRIOR PRIOR DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
SOFTWARE PALENTH VERSION 3.0
SEQ ID NO 27
LENGTH: 2026
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Best Local Similarity 93.4%;
Matches 1769; Conservative (
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                                                                                                                                                                                                                 Sequence 1, Application US/10343514

Publication No. US20040132025A1

GENERAL INFORMATION:
APPLICANT: ROSEN, Cheryl F.
APPLICANT: ROSEN, Cheryl F.
TITLE OF INVENTION: AMPR.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUCZ/PCT
CURRENT FILING DATE: 2003-01-31
PRIOR PELLING DATE: 2001-08-02.
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2000-08-03
PRIOR PELLING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/224,613
PRIOR PELLING DATE: 2001-03-12
PRIOR PELLING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-18
                                               GAATCCTTGGGGGGTAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTAC 1860
                                                                  GAATCCTTGGGGGGTAGCCGCTTTTCTCTGACAGACTGCCAAGAGGTGACAGCCTAC 1931
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Pred. No. 0;
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Best Local Similarity 93.4%;
Matches 1769; Conservative
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ORGANISM: RAT
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                                                                                                                                                                                                                                                                              Score 1360.2;
Pred. No. 0;
0; Mismatches
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 10/217,168
PRIOR FILING DATE: 2002-08-12
Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1884
                                                                                                                                                                                                                                                                              71.9%;
84.2%;
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Best Local Similarity 84.2
Matches 1565; Conservative
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APPLICANT: Libermann, Roadan K.
APPLICANT: Hunter; Ohn J.
APPLICANT: Hunter; Ohn J.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Gurtis, Rory A.J.
APPLICANT: Glandt, Peter J.
APPLICANT: Glavin, Katherine M.
APPLICANT: Glavin, Katherine M.
APPLICANT: Glavin, Katherine M.
APPLICANT: Glavin, Katherine M.
APPLICANT: Glavin, Mayoung
APPLICANT: Glavin
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                                                                                               1466 cecaaecricaegecrecrecrecarecaaaegearecreaaecreaareseaagrer
                                                                                                                                               CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT
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FILING DATE: 2000-11-15
PAPLICATION NUMBER: US 09/797,039
FILING DATE: 2001-02-28
APPLICATION NUMBER: US 60/186,061
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Publication No. US20040058355A1
GENERAL INFORMATION:
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707 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCATGGCACGTCCTTTGACG 766

APPLICANT: Curtis, Rory A.J. APPLICANT: Galvin, Katherine M.	TITLE OF INVENTION: 3/00, A NOVEL HUMAN FROTEIN KINASE AND USES THEREFOR FILE REFERENCE: 10147-50U1 CURRENT APPLICATION NUMBER: US/09/963,159 CURRENT FILING DATE: 2001-09-25		; SEQ ID NO 1 ; LENGTH: 3353 ; TYPE: DNA ; ORGANISM: Homo sapiens	; FEATURE: ; NAME/KEY: ungure ; LOCATION: (3268) ; NAME/KEY: ungure	; LOCATION: (3270) ; NAME/KEY: unsure ; LOCATION: (3272) US-09-963-159-1	Query Match 71.9%; Score 1360.2; DB 9; Length 3353; Best Local Similarity 84.2%; Pred. No. 0; Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps 2;	Qy         47 CCTCCGCCCTGGCCTCGGAGAGCGCCGGCGGCGGAGAGGGCTCATCAAGTCGCCTA 106	Qy 107 AACCTCTGATGAAGAGCGGGGTGAAGCGGCACCATCACAACACAACCTGCGGCACC 166	Qy 167 GCTACGAGTTCCTGGAGACGCTGGGCACCTACGGGAAGGTGAAGAAGGCACGAG 226	Qy         227 AGAGCTCGGGGGTCTGGTGGCCATCAAGTCAAAAATCAAAATGAAGATGAAGC 286	OY 287 AGGATCTGCTGCACATACGGAGGGAGTTGAGATCATGTCTTCACTCAACCCCCCCACA 346	Oy 347 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAAGATTGTGATTGTCATGGAGTATG 406	OY 407 CCAGCGAGGGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAG	Qy 467 CCAGGCATTTCTTCCGACAGATCGTGTCTGCCACCACCACCAGCAGGAACG 526	Oy 527 TTCACCGAGATCTCGAAAACATCCTTCTAGATGCCAATGGAACATCAAGATTG 586	Qy         587         CTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA         646           Db         731         CTGACTTCGGCCTCTCCCAACCTCTACGATCAAGGCAAGTTCCTGCAGACATTCTGTGGGA         790	647 GCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG	Db 791 GCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCCAGAGGTGG 850  Qy 707 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCGTGGTGGACCATGCCCTTTGACG 766
		TGGAGAATGGAGCCAAGGTGTGCA 1066 		SCTCAAAATCTGCAAGGTGACCCGG 1186                         SCCCAGTCTCTCCACAGTGACACGG 1174	TTAAGCTTCCGAAAGGCATTCTCA 1246                                       TCAAGCTGCCAAAGGCATTCTCA 1234	anggaccetcaggaactcagaccgg 1306 	CCCTGCTCCCAAGGAAAGCATCC 1366	rCTCTCCAGAGCCCAGCGAGTCTG 1426 	seggacccgrggagcagaagrcrc 1486 	NTTCTCAAACTCAATGGCAAGTTCT 1546 	TTGGCTCCCTGGACCAACTGGCCT 1606	SGGCTGTGAGTGAGGACAGCATCC 1666 	AACGTCTTCCCGAAACCCCACTGA 1726 	ABCCACCTCCTCAGAAG 1780	GGGATAGCTGCTTTTCTCTGACAG 1834 	TAGGAATCTGCTCAAGCTCAGC 1893 		
	947 GGGAACAGGAAGCCCTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGG 	1007 TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGG	1067 GCTTCTTCAAGCAGCACGTGCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCCTGGAGCTGTACCTGGGCTGGAGCCTGGAGCGGGGAAGCACCACCTGGAGCGGAAGCACCACCTGGAGCCACGTGGGGGGAAGCACCACCCTGGAGCGAAGCACACCACCTGGAGCGGAAGCACCACCTGGAGCGAAGCAAGC	1127 ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG	1187 CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA 1175 CTGATGACACTGCCCTGGCAAGAGCAACCTCAAGCTGCCAAAGGGCATTCTCA	1247 AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGG	1307 TGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCC	1367 TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCGAGCCCAGCGAGTCTG	1427 GGGAACTCTTAGACGCCAGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC	1487 CACAGGCTTCAGGGCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT	1526 CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCTTCCTCTTCGCTCCCTGGACGACCAACTCGCCCCCACCACCTTCGGCTCCCTGGATGAACTCGCCC	1607 CCTCCCATCCTGCAGCCCGGCCCCCCCTCAGGGGCTGTGAGTGA	1667 TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA	1727 GGGGCTGTGTGTGGACAAACCTGAGGGGCTTGAGCAGCCTCCCTC	1781GTCTGAAGCGATGGTGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCT	1835 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCT 		-09-963-159-1 Sequence 1, Application US/09963159 Patent No. US20020077312A1
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                        1835 ACTGCCAAGAGGTGACTGCAGCCTACAGCCCTAGGAATCTGCTCAAAGCTCAGC
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Best Local Similarity 84.2%; Pred. No. 0;
Matches 1565; Conservative 0; Mismatches 273; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
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ORGANISM: Homo Sapiens
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                                                                                                                                                                                                                                                                              .031 CCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGGGGCTACGCCACCCGAGTGG 1090
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851 ACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGCATGCCCTTTGATG 910
                                                                                                                                         AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGTGGTTAATGGTGAACCCCCACCCGTCGGG 886
                                                                          GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCA
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Db   1331 CTGATGACACTGCCCATCGCC   Qy   1247 AGAAAAGTCCTCTACCTGTC	Db 1562 GGGAGCTCTTGGACGCAGCGG  Qy 1487 CACAGGCTTCAGGGCTCCTCC  Db 1622 CGCAAGCTTCAGGGCTCCTCC  Qy 1547 CCCGCACAGCCTTAGAAGCA  Qy 1547 CCCGCACAGCCTTAGAGGCA  Qy 1607 CCTCCCATCCTGCAGCCCGGC  Qy 1607 CCTCCCATCCTGCAGCCCGGCC  Qy 1607 CCTCCCATCCTGCAGCCCGGCC  Qy 1607 CCTCCCATCCTGCAGCCCGGCC  Qy 1607 CCTCCCATCCTGCAGCCCGGGC  Qy 1607 TGTCCTCCGAGTCCTTTGACCJ	Db 1802 TGTCCTCTGAGTCCTTTGACCA Oy 1727 GGGGCTGTGTGTCTGTGGACA Db 1862 GGGCTGTGTTTTGACA Oy 1781GTCTGAAGCGATGGTC Db 1922 GAAGCTGCTGAGGCGTGGCC Oy 1835 ACTGCCAAGGGTGATCGGC Db 1982 ACTGCCAAGGGTGACTGCGGC	RESULT 10 US-10-311-034-38  Sequence 38, Application US/103110; Publication No. US20040023242A1 GENERAL INFORMATION: APPLICANT: INCTE GENOMICS, INC. APPLICANT: BARDICANT: BARDICANT: BARDICANT: BARDICANT: BARDICANT: BARDICANT: BOROWSKY, Mark L. APPLICANT: AU-YOUNG, Janice APPLICANT: BOROWSKY, Mark L. APPLICANT: CANDHI, Ameen R. APPLICANT: TRIBOULEY, Catherine APPLICANT: GREENWALD, Sara R. APPLICANT: GREENWALD, Sara R. APPLICANT: KEARNEY, Liam APPLICANT: KEARNEY, Liam APPLICANT: BUNGUN, Mariah R. APPLICANT: TANG, Y. TOM APPLICANT: BAUGHN, Mariah R.
		S87 CTGACTTTGGCCTCTCCAACCACAAGGCAAGTTCCTCCAGAGGTTTTGGGGA 646	
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TCAGGGGAGGTACAGGAGCCTCAGGAACTCAGACCGG 1306 CCTGTCCCTGCTGTATCCTGCTCCCAAGGAAAGGCATCC 1366 GAATCTGGTTACTACTCCTCCCAGAGCCCAGCGAGTCTG 1426 CTCCACCGCAAGGCATTCTCAAACTCAATGGCAAGTTCT 1546 TEGCAGGAATCCTTGGGGGATACCTGCTTTTCTCTGACAG 1834 CCTGGCAAGGAACCTCAAGCTGCCAAAGGGCATTCTCA 1390 ACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT 1606 GGGGCCCCCACCACCTTCGGCTCCCTGGATGAACTCGCCC 1741 CAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA 1726 CCCAGCCGCCCTCAGGGGCTGTGAGGACAGCATCC 1666 

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APPLICANT: THORNTON, Michael APPLICANT: HARALIA, April APPLICANT: HARALIA, April APPLICANT: Grandra S. APPLICANT: GURURALAN, Rajagopal APPLICANT: GURURALAN, Rajagopal APPLICANT: KHAH, Farrah A. APPLICANT: REGIPON, Shirley A. APPLICANT: AZIMZAT, Yalda APPLICANT: BLIOTT, Vicki S. APPLICANT: BATRA, Sajeev APPLICANT: BATRE: 2002-12-10 AUBBER OF SEQ ID NOS: 52 SOFTWARE PELL PROGRAM SEQ ID NOS: 52 SOFTWARE: BATURE: ARATURE: ARATURE: ARATURE: ATURE: ARATURE: ATURE: ATUR	Dest Match   1.7.7;   Score 1357.6;   De 16;   Length 1380;

	500 CCAGCCGGGGCACCTTTATGACTACATCAGCGGCGCGCGC	620 TCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGGATGCCAATGGGAATATCAAGATTG 679  587 CTGACTTTGGCCTCTCCAACCTGTACCAAAGCCAAGTTCCTCCCAGACGTTCTGTGGGA 646  680 CTGACTTCGGTCTCTCCAACCTCTACCATCAAGGCAAGTTCCTGCAGACATTCTGTGGGA 739  647 GCCCTCTCTACGCCTCGCCTGAGATGTCAACGGAAGCCCTATGTGGGCCCAGAGGTGG 706  11	ACAGCTGGTCTCTGGGCGTTCTCTGTACATCCTGGTGCATGGCCACCATGCCCTTTGACG		947 GGGAACAGGAAGCCCTGCGTGAGGGTGGCACCTAGTGGTGACTTTGGCCGGCC	1067 GCTTCTTCAAGCAGCAGCAGGAAGCACTGTACCTGGGCTGGAGCGGCAAC	1187 CTGAGGATACCTCTTCTCGCCTGGCAGGCGCTTAAGCTTCCGAAAGGCATTCTCA 1246
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	1727 GGGGCTGTGTGTGTGGACAACCTGAGGGGGCTTGAGCGCCCCCAGAGGGGGGCTTGAGGCCTCCCTC	OY 1835 ACTGCCAAGAGGTGACTGCACCTAAGGAATCTGCTCAAGCTAGG 1893	GENERAL INFORMATION:  APPLICANT: Tang, Y. Tom  APPLICANT: Drmanac, Radoje T.  TITLE OF INVENTION: Polypeptides  TITLE OF INVENTION: Polypeptides  FILE REFERENCE: 803 1.0NCP  CURRENT APPLICATION NUMBER: US/10/302,172	PRIOR APPLICATION NUMBER: US 10/225,251   PRIOR FILING DATE: 2002-08-20   PRIOR FILING DATE: 2002-08-20   PRIOR FILING DATE: 2002-03-05   PRIOR FILING DATE: 2002-03-05   PRIOR FILING DATE: 2001-03-05   PRIOR FILING DATE: 2001-03-05   NUMBER OF SEQ ID NOS: 950   SOFTWARE: DE FL Genes Version 2.0	215- 22501 A : Homo sapiens : CDS : (106) . (1989)	1.6%; Score 1355.4; DB 16; Length 2501; 4.0%; Pred. No. 0; ve 0; Mismatches 276; Indels 21; Gaps CTCGGAGAGCGCCGGCCGTGGCGACGGCTATCAAGTCGCTA	DD 140 CCACTCCCTCGGCCGCGCCGCCGCGCGCGGAAGGCCTGATCAAGTCGCCCA 199  Qy 107 AACCTCTGATGAAGAAGCGGCGGTGAAGCGCCCATCACAACCACCACCACCACCACCACCACCACCACCA

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CCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGGCTGATCAAGTCGCCCA
                                     227 AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC
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PRILICANT: BODARY, SARAH C.
PAPLICANT: CLARK, HILLARY
APPLICANT: SCHORNELL, HUNTE
APPLICANT: SCHORNELD, JILL R.
APPLICANT: WOLDANGE, MICKEY
APPLICANT: WOOD, WILLIAM, I.
APPLICANT: WO, WILLIAM, I.
APPLICANT: WO, THOWAS D.
TITLE OF INVENTION: Compositions and Methods for the Tree;
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,7158
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 639
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US-10-370-715B-639
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Sequence 13, Application US/10343514

Publication No. USZO040132025A1

GENERAL INFORMATION:

APPLICANT: DRUCKER, Daniel J.

APPLICANT: DRUCKER, Dainel J.

APPLICANT: LEFEBURE, Diana L.

TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK

FILE REFERENCE: DPA-DRUCZ/PCT

CURRENT PEPLICATION NUMBER: US/10/343,514

CURRENT PELING DATE: 2003-01-31

PRIOR FILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-28

NUMBER OF SEQ ID NOS: 109

SOFTWARE: Patentin version 3.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 1, Application US/09984890

Patent No. 6492156

APPLICANT: VAN. Chunhua et al.

TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: THEREOF

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TITLE OF INVENTION: THEREOF

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                                                                                                                                                                                                                                          Score 202.6; DB 4; Length
Pred. No. 2.1e-47;
0; Mismatches 344; Indels
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2175
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Best Local Similarity 54.9
Matches 422; Conservative
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US-09-984-890-1
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REPRENCE: CLOO1306D1V
CURRENT APPLICATION NUMBER: US/10/274,194
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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RESULT 6 US-09-270-767-1257/c

US-10-274-194-1
; Sequence 1, Application US/10274194
; Patent No. 6706511
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.

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323 412 263 472 203 592

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Sequence 1. Application US/09930181

Sequence 1. Application US/09930181

Patent No. 6455292

GRNERAL INFORMATION:

GRNERAL INFORMATION:

TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas CURRENT PILINE DATE: 2001-08-16

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin version 3.0

SEQ ID NO. 1
                                                                                                                          442 CCGGCCAGGAGGTGGCTATCAAAACCATCAAGAGTGCAAGATCGAGGCCGAGGCGGATT 383 😁
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                                                                233 CGGGGGGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCAGGATC 292
                                                                                                                                                                                       TGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACATCATTG 352
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      Mismatches 158;
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Pred. No. 1e-42;
0; Mismatches 356;
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Best Local Similarity 53.5%;
Matches 413; Conservative
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US-09-930-181-1
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ORGANISM: Homo sapiens
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US-09-930-181-1
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APPLICANT Homburger et al.

TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogaster

TITLE OF INVENTION: Nuclei acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
                                                                                       APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 1257
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Pred. No. 6.2e-44;
0; Mismatches 158;
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; Sequence 16539, Application US/09270767
; Patent No. 6703491
Sequence 1257, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1257

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al Similarity 64.3%;
284; Conservative
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ORGANISM: Drosophila
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Best Local Similarity
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LENGTH: 484
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Best Local Similarity
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Batent No. 6258547

GENERAL INFORMATION:
APPLICANT: Beri, Rajindar K.
APPLICANT: Carling, David
APPLICANT: Porder: Robert A.
TITLE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINA FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT PILLOR DATE: 1996-03-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-06-31
PRIOR FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOSPTWARE: PatentIn Ver. 2.1
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APPLICANT: Carling, David
APPLICANT: Porder, Robert A.
TITLE OF INVENTION: WUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-030-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
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Pred. No. 1.3e-41;
0; Mismatches 381;
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                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: cDNA of CTHER INFORMATION: liver AMP protein kinase US-08-557-006C-24
                                                                                                                                                                                                                                    Score 182.4; DB 3; Length 2761;
Pred. No. 1.3e-41;
0; Mismatches 381; Indels 6;
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      PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-06-31
PRIOR FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 53.0%;
Matches 437; Conservative
                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Seguence
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Sequence 38, Application US/08557006C
Batent No. 6258547
GENERAL INROPARATION:
APPLICANT: Carling, David
APPLICANT: Carling, David
APPLICANT: Carling, David
TILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C
CURRENT FILING DATE: 1996-03-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR PILING DATE: 1994-05-20
PRIOR PAPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1994-05-20
PRIOR PILING DATE: 1993-08-31
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Local Similarity 53.1%; Pred. No. 2.3e-41;
les 434; Conservative 0; Mismatches 378;
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719 407 467

839 527 899 959 647 707

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1080 TGTGTGGAGTCTTGTTTTATACACTAGTCAGTGGCTCACTTCCCTTTGATGG 1139
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                                                                                                                                                                                                                                                    779
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   600 TATCCTTACAGGCAGAGGTTGCAATAAAATAATTGACAAACTCAGTTGAATCCAAC 659
                                                                                                                                                                                                                                                 720 AGTGAAGTTATTCGAAGTCATTGAAACTGAAAAACACTCTACCTAATCATGGAATATGC
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                                                                288 GGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACAT
                                                                                                                             660 AAGTCTACAAAAGCTCTTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATAT
                                                                                                                                                                                       348 CATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGC
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION WUMBER: US/09/774,528

CURRENT FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 441
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Patent No. 6743619
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Zhou, Ping
Goodrich, Ryle
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Zhao, Qing A.
Yang, Yonghong
Xue, Aidong J.
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Wang, Jian-Rui
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Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren, Feiyan
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CGTICTCCTGTACATCCTGGTGCATGCCATGCCCTTTGACGGGCAGGATCATAAAAC 782
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                                                                                                                       ACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATGCCTG 842
                                                                                                                                                                                                                                              TGGC----CTGATCCGGTGGCTGTTAATGGTGAACCCCACCCGTCGGGCCACACTGGAGGA 899
                                                                                                                                                                                GCTCTTTAAGAAGATCCGAGGGGGTGTCTTCTACATCCCGGAGTATCTCAACCGTTCTAT 722
                                                                                                                                                                                                                                                                                                       récearcrécreardeacarderecaderesacécerreaasceasecaderareaasa 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cracagacrerricaaaacaarcescaaeeegaarrrrecaaaaeraaarreecaaeaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Piwnica-Worms, Helen
TITLE OF INVENTION: DNA SEQUENCES ENCODING HUMAN TCAK-1
TITLE OF INVENTION: KINASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSE ADDRESSEE: ADDR
                                                                                                                                                                                                                                                                                                                                                                                                                              783 CATACGAGAGCATGAATGGTTTAAACAGGATTTGCCCA 820
                                                                                                                                                                                                                                                                                                                                                                     900 TGTAGCCAGTCATTGGTGGGTCAACTGGGGGTTACACCA 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPACTIBLE
OPERATING SYSTEM: PC PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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Pred. No. 7.2e-
0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,298
FILING DATE: 09-UUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: CACULHERS, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 9-96
TELECPHONE: (303) 499-8080
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08677298
Patent No. 5863729
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US-08-677-298-1
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Best Local Simi
Matches 404;
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; NAME/KEY: CDS
; LOCATION: (482)..(2239)
US-09-930-181-3
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                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3364
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SOFTWARE: pt_FL_genes Version 2.0 SEQ ID NO 112 LENGTH: 2899
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Best Local Similarity 52.4%;
Matches 412; Conservative
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US-09-774-528-112
                                                                                                                                                              ORGANISM: Homo sapiens
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RESULT 14 US-09-930-181-3

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Sequence 3, Application US/09930181
Patent No. 6455292
GENERAL INFORMATION:
APPLICANT: Origene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REPERENCE: 160 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO
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9.2%; Score 174; DB 4; Length 33
Best Local Similarity 53.4%; Pred. No. 3.6e-39;
Matches 414; Conservative 0; Mismatches 355; Indels
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1000 ACGCCCCCCCACCCTAGAGCACATTCAGAAACACATATGGTATATAGGGGGCCAAGA 1055
                                                                          US-10-003-690-3

Sequence 3, Application US/10003690

Patent No. 6787345

GENERAL INFORMATION:

APPLICANT: ROTY A.J. Curtis

TITLE OF INVENTION: 55053, A No. 6787345el Human Eukaryotic Kinase

TITLE OF INVENTION: and Uses Therefor

FILE REFERENCE: MNI-206

CURRENT APPLICATION NUMBER: US/10/003,690

CURRENT FILING DATE: 2001-11-15

PRIOR APPLICATION NUMBER: 60/248,893

FRIOR FILING DATE: 2000-11-15

NUMBER OF SEQ ID NOS: 8

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 3
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9.1%; Score 173; DB 4; Length 2334;
Best Local Similarity 52.7%; Pred. No. 5.8e-39;
Matches 399; Conservative 0; Mismatches 355; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: (1)...(2334)
US-10-003-690-3
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Oy 824 --CCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGTTTAATGGTGAACCCCACCG 881

Db 756 CTTCATTCCTCCAGATTGCCAGACTCCTGAGGGAATGATCGAAGTCGAAGACCGGAAA 815

Oy 882 TCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTG 918

Db 816 AAGGCTCATTGGTGAGCAATTCAGAGG 852

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IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4134886 seqs, 2624710521 residues Searched:

8269772 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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genesequ1980s:\*
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## ALIGNMENTS

RESULT 1

Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder; wound healing; periodontal disease; inflammatory disease; tumour; infection; allergy; ss. Murine Lymph node Stromal cell kinase 1 coding sequence. Martin U, Anderson DM; ВР. AAC90433 standard; cDNA; 2902 26-MAY-2000; 2000WO-US014696. 99US-0136781P. 19-MAR-2001 (first entry) (IMMV ) IMMUNEX CORP. Virca GD, WO200073468-A1. 28-MAY-1999; Mus musculus. 07-DEC-2000. AAC90433; Bird TA, AAC90433 

Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.

WPI; 2001-061546/07. P-PSDB; AAB50056.

Claim 1; Page 86-87; 106pp; English.

The present sequence is the coding sequence for Murine Lymph node Stromal cell kinase 1 (MLSK-1). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, mayeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal infection

2902 BP; 654 A; 794 C; 796 G; 658 T; 0 U; 0 Other;  100.04; Score 1893; DB 4; Length 2902;  25. Conservative 0; Mismatches 0; Indels 0; Gaps ATGGAGTGGTGGCTTACTCCAGCGCCGAGCTCCTCGGCCCTCGGCCTCGGCCCTCGGCCCTCGGCCCTCGGCCTCGGCGCCTCGGCGCCTCGGCGCCTCGGCGCCTCGGCGCCTCGGCGCCTCGGCGCCTCAGCAGCCTCGGCGCCTCAGCAGCTCGGCGCCTCAGCAGCCTCGGCGCCTCAGCAGCCTCGGCGCCTCAGCAGCCTCGGCGCCTCAGCAGCCTCGGCGCCTCAGCAGCCTCGGCGCCTCAGCAGCAGCTCAGCAGCTCGGCGCCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCTCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
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The invention relates to an AMPK (AMP-activated protein kinase)-related kinase, designated SNARK polypeptides and polymucleotides. SNARK contracted protein kinase) is involved in stress response to glucose deprivation. The polymucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK protein in isolated form or as a protein conjugate. Activation of SNARK in catal and in the catal and selects and selects and selects and selects that would enhance the disposal of glucose to have insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipopycerides. SNARK or its variants may be administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as diabetes. SNARK antibodies are used to modulate SNARK activity either in vivo for therapeutic purposes. SNARK antagonists may be administered to increase the surface of in vitro, for drug screening and related investigational purposes. SNARK antagonists may be administered to increase full propose in a partiant decrease divides intake and increase levels of blood of linose in a partiant.
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Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes; glucose deprivation; lipid metabolism; therapy; lipoprotein disorder; hyperglycaemic; drug screening; hypoglycaemia; ss.
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12-MAR-2001; 2001US-0274613P.
28-MAR-2001; 2001CA-02340783.
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cell proliferation; cell differentiation; cell growth; cell division;
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                                                                                                               US2004058355-A1.
                             human; gene; ss.
                                                                      Homo sapiens
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22-OCT-2002;
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05-OCT-1999
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      Antiarchritic; antiarcheumatic; neuroprotective; antiniflammatory;
antiarchritic; antiarcheumatic; cardiovascular; virucide; analgesic;
A matipsoriatic; antiasthmatic; cardiovascular; virucide; analgesic;
A majogenesis inhibitor; anglogenesis stimulator; cerebroprotective;
A majogenesis inhibitor; anglogenesis stimulator; cerebroprotective;
A majogenesis inhibitor; anglogenesis stimulator; cerebroprotective;
A majogenesis inhibitor; antithyroid; dermatological; immunomodulator;
A majogenesis sell disorder; ceal differentiation disorder;
A brain disorder; platelet disorder; places disorder;
A central disorder; cervical disorder; spleen disorder; thymus disorder;
A modothelial disorder; skeletal muscle disorder; thymus disorder;
A metabolic disorder; cardiovascular disorder;
A metabolic disorder; love metabolism disorder;
A metabolic disorder; neurological disorder;
A metabolic disorder; neurological disorder;
A blood vessel disorder; anglogenic disorder;
A blood vessel disorder; anglogenic disorder;
A propertension; anglina; osteoarthritia; rheumatoid arthritis;
A multiple sclerosis; Crohn's disease; psoriasis; asthma;
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                                                                                                    1501 CTCCTCCTCCACGCAAGGGCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCTTA 1560
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                                                                                                                                                             CAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGAC 1440
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                           CCCTCATCGGGGGGGGTACAGGAGGGCCCTCAGGAACTCAGACCAGTGTCCAATACCCCA 1402
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                                                                                                                                                                                                                                                                        cytostatic; cardiant; hypotensive; antianginal; osteopathic;
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The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising polypeptides are useful for diagnosing and treating a subject having a disorder, or a subject at risk of developing a disorder, which is associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.
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Chun M, Williamson MJ;
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Galvin KM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kapeller-Libermann R, Hunter JJ,
Curtis RAJ, Olandt PJ, Tsai F,
Silos-Santiago I, Bandaru R;
                                               99US-00163821.
99US-0117580P.
99US-00276400.
99US-00365162.
99US-00392189.
                                                                                                                                                                                                                                                                                                                                                      2000US-0234922P.
2000US-023603SP.
2000US-024663P.
2000US-0211216.
2000US-0248325P.
2000US-0257511P.
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2001US-00797039.
2001US-00845044.
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2001US-00920346.
2001US-00928531.
2001US-00929218.
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2001US-00963159.
2001US-00008016
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2001US-00003690
2002US-00060763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002US-00105989
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25-APR-2003; 2003US-00423543
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m1983, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 activity, such as cellular proliferative and/or differentiative disorders, brain disorders, platelet disorders, breast disorders, colon disorders, kidney (renal) disorders, long disorders, prostate disorders, cervical disorders, spelen disorders, prostate disorders, cervical disorders, spelen disorders, phymus disorders, thyroid disorders, skeletal muscle disorders, chematopoietic disorders, parceatic disorders, skeletal muscle disorders, skin (dermal) disorders, disorders, cardiovascular disorders, minume, e.g. inflammatory disorders, cardiovascular disorders, pain disorders, neurological or central nervous system disorders, erythroid disorders, neurological or central nervous system disorders (all disorders, neurological or central nervous system disorders (all claimed), e.g. cancer, heart failure, hypertension, angina, osteoarthritis, rheumatoid arthritis, multiple sclerosis, Crohn's disease, psoriasis, or asthma. The nucleic acid molecules and polypeptides are also useful as modulating agents in regulating a variety division. This sequence encodes a novel human protein of the invention.

Note: The sequences given in the specification are also avaialable in the sequences and process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355.
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Sequence 1884 BP; 403 A; 599 C; 548 G; 334 T; 0 U; 0 Other;

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	2;	106	94	166	154	226	214	286	274	346	334	406	394	466	454	526	514	586	574	646	634	902	694	166
339 () 348 6; 334 1	Query Match 71.9%; Score 1360.2; DB 12; Length 1884; Best Local Similarity 84.2%; Pred. No. 0; Matches 1565; Conservative 0; Mismatches 273; Indels 21; Gaps	47 CCTCCGCCCTGGCCTCGGAGGGCGCCCGGCTGGCGACGGGCTCATCAAGTCGCCTA	5 CCACTCCGCCGCGGCGGCTAGCCCGGCCGGAGGGGGGGGG	107 AACCTCTGATGAAGAAGCAGCGGTGAAGCGGCACCATCACAAACACACAC	95 AGCCCCTAATGAAGAAGAAGCGGCGACCACCACCACCAAGCACAACCTGCGGCACC	7 GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAG		227 AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC	215 AGAGCTCGGGGCCCTGGTCGTCAAGTCAATCCGGAAGGACAAAATCAAAGATGAGC	287 AGGATCTGCTGCACATACGGAGGAGGATTGAGATCATGTCTTCACTCAACCACCCCCACA				7 CCAGCGGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAG		7 CCAGGCATITCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACAGAACGGGATCG		7 TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG		7 CTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA		7 GCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGGCCCCAAGGTGG	635 GCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGGAAGCCCTACACAGGCCCAGAGGTGG	707 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACG
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The present invention relates to the isolation of a novel human protein kinase designated 3700, and the polymucleotide sequence encoding it. The invention also describes the use of a modulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a subservate protein. Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylation, cell signalling, tumourigenesis, mitogenesis, transcription of a gene, and progression of atherosclerosis, and signalling across the blood-brain barrier. The polymucleotide and signalling across the blood-brain barrier. The polymucleotide and solypeptide molecules for protein kinase 3700 may be used as diagnostic targets and therapeutic agents for prognosticating, diagnosing, preventing, inhibiting, alleviating, or curing PK-related disorders and callular proliferative and/or differentiative disorders and callular proliferative and/or differentiative disorders and callular proliferative and/or carcinoma, metastatic disorders or leukaemia). The 3700, to carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700, to detect a genetic alteration in a 3700 gene, in chromosome mapping, for
GAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGGACAGCTGCTTTTCCCTGACAG 1825
                                                                                                                                                                                                                                                                                                                                           Human; protein kinase 3700; PK; protein phosphorylation; tumourigenesis; cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma; cissue repair; tissue regeneration; atheroselerosis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia;
                                                               ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
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/*tag= a
/*product= "Protein kinase 3700"
/product= "The coding region (not including the terminator codon) is specifically claimed in claims 7 and 28"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; antiatherosclerotic; gene; ss
                                                                                                                                                                                                                                                                                                       cDNA encoding human protein kinase 3700
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                                                                                  Sequence 3353 BP; 754 A; 1022 C; 879 G; 695
tissue typing, in forensic biology, and as sequence encodes human protein kinase 3700
                                                                                                                                     Score 1360.2;
Pred. No. 0;
                                                                                                                                                                                          0; Mismatches
                                                                                                                                     71.9%;
84.2%;
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Best Local Similarity
Matches 1565; Conserv
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New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, failure and angina. 2004-268788/25 WPI; 2004-268788/ P-PSDB; ADL14161 

Claim 1; SEQ ID NO 43; 139pp; English

The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 21970, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and colypeptides are useful for diagnosing and treating a subject having a disorder, which is associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501, 27903, 3700, 21529, 26176, 26344, 55053, 2504, 15977, 14760, 25501, 26343, 38555 or 593 activity, such as cellular proliferative and/or disorders, colon disorders, kidney (renal) disorders, prostate disorders, prostate disorders, prostate disorders, prostate disorders, testes disorders, canorders, canorders, prostate disorders, testes disorders, canorders, canorders, canorders, pancreatic disorders, pancreatic disorders, disorders, disorders, skeletal muscle disorders, disorders, disorders, cardiovascular disorders, pancreatic disorders, real disorders, canorders, canorders, pain disorders, disorders, cardiovascular disorders, pain disorders, disorders, cardiovascular disorders, canorders, art failure, hypertension, angiogenic disorders, are also useful as modulating agents in regulating a variety of cellular process, e.g. cell proliferation, differentiation, growth and division. This sequence encodes a novel human protein of the invention. Plactronic forms. ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355 electronic format

Sequence 3353 BP; 754 A; 1022 C; 879 G; 695 T; 0 U; 3 Other;

106 166 310 286 430 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCACAAA 346 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406 610 GCTACGAGITCCTGGAGACCCTGGGCGAAGGCACCTACGGGAAGGTGAAGAAGGCGCGGG CCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGGCTGATCAAGTCGCCCA CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA **AGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACACAAGCACAAACCTGCGGCACC** GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAAGGCACGAG AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC TCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTGATCGTCATGGAGTATG ccaecceaecearcerrareacracarcaaccaaccaecaecracaeraeae AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACC Gaps DB 12; Length 3353; 21; Score 1360.2; DB 12; Lengtl Pred. No. 0; 0; Mismatches 273; Indels Query Match
Best Local Similarity 84.2%;
Matches 1565; Conservative 191 251 167 227 47 101 311 371 287 431 347 491 407 551 셤 셤 g g ద ò 요 8 ઠે 8 ò ò ઠે

1390 1606 1186 1306 1366 1546 1681 1006 1210 1126 1270 1330 1426 1486 1030 1090 1066 1391 AGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTACAGGAGCACCCTCCGGAGCTCAGCCCAA 1450 1501 1561 1621 646 790 910 886 946 670 586 730 706 850 996 826 970 AGAAAAAGTCCTCTACCTCGTCAGGGGGGGGTACAGGAGGACCCTCAGGAACTCAGACCGG CCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCG CTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGCCATCAGAACAGAGTTG TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG rccacceadarcrcaaccredadaacarccrcrredarccaareccaararcaacarre CTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA creactresecercreacereracearcaasseaastreerseasacareresesa GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCCAGAGGTGG GCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGCCCAGAGGTGG ACAGCTGGTCTCTGGGCGTTCTCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACG Acaderacereceredenterecretacarecredendendendendendente GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCA GGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCCTACCGGGAGCCATA AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCCACCCGTCGGG .031 ccacccrigaaggargragccagrcacrigargarcaacrigaggcracgccacccaagrag GGGAACAGGAAGCCCTGCGTGAGGGTGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCA GAGAGCAGGAGGTCCGCATGAGGGTGGGCACCTGGCAGTGACTCTGCCCGCGCCTCA GCTTCTTCAAGCAGCACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAAC <u>ectricirica a de caraca con con esta a concerció de a contra a co</u> ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG CTGAGGATACCTCTTCTCGCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA creargacacreccarceccreecaagaecaaccreaaecreecaaageecarrerea TGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCC TCCCTGCGAGCCCAGGCTGCCC-----CCCTGCTCCCCAAGAAGGGCATTC TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCCAGAGCCCAGGGGTTTG 1427 GGGAACTCTTAGACGCCAGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC GGGAGCTCTTGGACGCGACGTGTTTGTGAGTGGGGATCCCAAGGAGCAGAAGCCTC CACAGGCTTCAGGGCTCCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT 1547 CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCTCCTGGAGATGGAGCCAAGGTGTGCA CGCAAGCTTCAGGGCTCCTCCATCGCAAAGGCATCCTCAAACTCAATGGCAGCTTCT 671 731 647 791 707 827 971 1001 1001 1067 1211 1271 1187 1331 1247 1307 1451 1367 1502 1562 1487 467 611 527 587 851 767 911 887 947 1127 셤 ò g ò 셤 δ g à g 8 임 ð 셤 ò g ò g à g ð 요 à 요 ò 셤 ò g ò 셤 8 g à 셤 ò g ò Ë

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Thangavelu K,

Elliott VS,

Grether M,

WPI; 2002-090207/12. P-PSDB; AAE16266.

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Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y; Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR; Ramkumar J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang YT; Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R; Lo TP, Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L;

(INCY-) INCYTE GENOMICS INC.

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human toxicity
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                                                                                                                                                                                                  New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.
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Parch 3360; Score 1357.6; DB 6; Length 3360;
Best Local Similarity 83.7%; Pred. No. 0;
Matches 1569; Conservative 0; Mismatches 284; Indels 21;
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                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 184; 197pp; English
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	Qy         1820 GCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAAGCCCTAGGAATCT 1879           Db         1889 GCTTTTCCCTGACAGCTGCCAGGAGGTGACGGACCTACCGACGTCT 1948           Qy         1880 GCTCAAAGCTCAGC 1893           Db         1949 GCTCAAAGCTCAGC 1962	SUL K94	AC AAK94280; XX DT 06-NOV-2001 (first entry)	AX DE Human full-length cDNA, SEQ ID NO: 2918. XX XW Human; full length cDNA; cDNA synthesis; oligo-capping; ss.	AX AX OS Homo sapiens. XX PN EP1130094-A2.	XX PD 05-SEP-2001. XX PF 07-JUL-2000; 2000EP-00114089.	XX	X RES INST. ikawa T, Igogai T, Hayashi K, Ishii S, Kawai Y;	waxamatbu A, Suglyama 1, Nagal K, Kojima S, OCBUKi WPI; 2001-524255/58. P-PSDB; AAM93360.	830 Primers useful for synthesiz in genetic manipulation.			CC libraries that were synthesised by the oligo-capping method. The primers CC enable the production of the full length cDNA easily without any special CC enable. The present sequence is a full length human cDNA of the CC invention. Note: The sequence data for this patent did not form part of CC the printed specification, but was obtained in CD-ROM format directly	CC from BPO
Qy         512 ACCAGAACGGGATCGTTCACCGGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATG         571           Db         578 ATCAGAACGGATTGTCCACCGGGAGATCTCAAGCTGGAACATCCTTTGGGTGCCAATG         637           Cy         572 GAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACACAAAGGCAAGTTCCTCC         631           Db         638 GGAATTGCTGACTTTGGCCTCTCCCAACCTGTACCATCAACGGAAGTTCCTGC         697           Qy         632 AGACTTCTGTGGGACCCTCTCTACGCTTCCAACCTCTACCATCAACGGAAGCCTATG         691           Bb         698 AGACTTCTGTGGGAGCCCTCTCTATGCCTCGCCTGAGATTGTCAATGGGAAGCCTATG         757           Qy         692 TGGGCCCAGAGGTGGACCCTCTTGTGGGGTTCTCCTGTACATGGGAAGCCTTACATGGTAATGGAGATGTCAATGGCAATGGCAAGATGATGAAAAAAAA	752 CCATGCCCTTTGACGGCAGGATCATAAACACTGGTGAAGCAAATCAGTAACGGGGCTT	872 ACCCCACCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGGTT	Db 998 ACCCCCCCGAGTGGGAGAGCTCCCCCTTGTGGGGTGGGG	Qy         992         TTGGCCGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGGGCCCCTCCTGGAAATG         1051           Db         1058         CTGCCCGGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCCTCCTGGAGAATG         1117	Oy         1052         GAGCCAAGGTGTGCACTTCTTCAAGCAGCACGTGCGGGAGGTGGAAGTGTACCTG         1111           Db         1118         GGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGAAGCACCACCCCTG         1177	QY     1112     GGCTGGAGCGCAACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATC     1171       DD     1178     GCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCAGTCTC     1237	QY     1172 TGCAAGGTGACCGGCTGAGGATACCTCTTCTCGCCCTGGCAAGAGCAGCCTTAAGCTTC 1231       DD     1238 TCCACAGTGACACGGCTGATGACACTGCCCATGGCAGCAAGCTGC 1297	Qy     1232     CGAAAGGCATTCTCAAGAAAAAGTCCTCTACCTCGTCAGGGAGGTACAGGAGGACCCTC     1291       Db     1298     CAAAGGCATTCTCAAGAAAGGTGTCAGCCTCTGCAGAAGGGTACAGGAGGACCCTC     1357	Qy         1292         AGGAACTCAGACGGGGCCTGATACTCCAGGGCAGCCTGTCCTGCTGTTCCCTGCTCC         1351           Db         1358         CGGAGCTCAGCCCAATCCCTGCAGGCCAGGGCAGCTGCCCCCCTGCTCC         1408	Qy     1352     CAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCAG     1411       Db     1409     CCAAGAAGGCCATTCTCAAGAAGCCCCGACAGCGGAGTCTGGCTACTACTACTCCTCCCC     1468	Qy     1412 AGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATGTTTTGTGAGTGGGACCCCG     141	Qy     1472     TGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCCTCCTCCACAGGCATTCTCAAAC     1531       Db     1529     AGGAGCAGAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAAC     1588	532 TCAATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCC	1592 IGGACCAACIGGCCICCCATCCIGCAGCCCAGCCGCCCCTCAGGGGCTGTGA 1651

Que Bes Mat	quence Match Local S es 1563	8 8 8 8	1112 TGGCTGACTCGCGCGTTCCTCCGCCCCCTCGAGAATGGGGCCAAGGTGTGCA 1171  1067 GCTTCTTCAAGCAGCACGTGCCGGGAAGCACTGTACCTGGGGTGGAGCGCCAAG  1172 GCTTCTTCAAGCAGCATGCACCTGGGGGAAGCACCCCCTGGCCTGGAGCGCCAGC 1231  1172 GCTTCTTCAAGCAGCATGCACTGGGGAAAGCACCACCCTGGCCTGGAGCGCCAGC 1231  1127 ATTCTTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAAATGACCAGCATGACACACAGAACAACAAAATGACAAAATGACAAAATGACAAAATGACAAAATGACAAAAATGACAAAATGACAAAATGACAAAAATGACAAAAATGACAAAAATGACAAAAAAAA
g & g	152 CCACTCCCTCGGCCGCAGAGCTAGCCCGGCTGGCGGAAGGCTGATCAAGTCGCCCA 211 107 AACCTCTGATGAAGAAGCAGGCGGTGAAGGCGCATCACAACACACAACCTGCGGCACC 166 1	, vo 40	CTGAGGATACCTCTTCTGGCCAAGAGCAGCCTTAAGCTTCGAAAGGCATTCTCA
දු පු	GCTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAGGCGGGGGGGG	<i>ò</i> 8	
& 93	227 AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGAAAGACAAAATCAAAGATGAGC 286 	& 8 	
ç D	287 AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAC	රු යි 	1367 TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTG 1426 
oy Og	347 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406 	<b>상</b> 옵	
දු දු	407 CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAG	<b>상</b> 옵	1487 CACAGGCTTCAGGGCTCCTCCTCCACGCAGGGCATTCTCAAACTCAATGGCAAGTTCT 1546 
λ O		<i>ò</i> 8	1547 CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT 1606 
oy Db	TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG	8 &	1607 CCTCCCATCCTGCAGCCCGGCCCCTCAGGGGCTGTGAGTGA
S SS	CTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCCAGACGTTCTGGGAAATTCCTCCAACCTTCTCAACCTCTACCATCCAACCTCTACCATCCAACCTTCTGAAAATTCTGAAAAATTCTGAAAAATTCTGAAAAATTCTGAAAAATTCTGAAAAAATTCTGAAAAAATTCTGAAAAAAAA	& 8	1667 TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA 1726
oy Dp		& 8 8	1727 GGGGCTGTGTGTCTGTGGACAACCTGAGGGGGCTTGAGCACCTCCCTC
b 6y		<i>≿</i> 8	1781GTCTGAAGCGATGGTGGCAGGAATCCTTGGGGATAGCTGCTTTTCTCTGACAG 1834 
oy Oy	GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCGCCCA	<i>ኤ</i> ଶ	1835 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893 
දු පු	827 AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCGTCGGG 886	RESUL ADL30 ID	T 8 885 ADL30885 standard, cDNA, 3395 BP.
<b>상</b> 음	887 CCACACTGGAGGATGTAGCCAGTCATTGGTGGGGTCAACTGGGGTTACACCGCGGAGTCG 946	XX A XX DI XX A DI XX	20-MAY-2004 (first entry)
송 원	947 GGGAACAGGAAGCCCTGCGTGAGGGAGCACCCTAGTGGTGACTTTGGCCGGGCCTCCA 1006	<b>%                                    </b>	l] nan
ò	1007 TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCCTCCTGGAGATGGAGCCAAGGTGTGCA 1066	XX XX OS	oligo-capping method; ss; gene. Homo sapiens.

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CTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTGCAGACATTCTGTGGGA
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S, Otsuki
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Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-001183865.
07-JUL-2000; 2000EP-00114089.
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screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, extation and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antifilammatory activities. This polynucleotide sequence is a human kinase DNA sequence
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                                                                                                                                                                                                                                                                                                                          gene; ds; kinase; human; SNP; single nucleotide polymorphism; tyrosine protein kinase; serine/threonine protein kinase; PTK; STK; gene therapy; cancer; immune-related disease; cardiovascular disease; brain; neuronal associated disease; metabolic; inflammatory disorder; cytostatic; neuroporcective; immunomodulator; antinflammatory; calcium/calmodulin-dependent protein kinase; NuaK2.
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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes

(first entry)

20-JAN-2003

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ABZ11333 standard; cDNA; 2043

RESULT 10 ABZ11333 ID ABZ1 XX AC ABZ1

ABZ11333

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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ1119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, in diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
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                                                                                                                                                                                                                      Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet or coagulation disorders.
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cell-proliferative disorder; neurodegenerative disease; bacterial;
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Pred. No. 0;
0; Mismatches 276;
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I Y, Yamazaki V, Chen R,
Wang D, Drmanac RT;
                                                                                           Human polynucleotide SEQ ID NO 215
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Best Local Similarity 84.0%;
Matches 1562; Conservative
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T, Wang J,
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05-MAR-2002; 2002WO-US005095.
20-AUG-2002; 2002US-00225251.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM43851 standard;
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(DRMA/) DRMANAC R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ss; gene; human; genetic disorder.
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                                                                     AGGATCTGCTGCACATACGGAGGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA
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The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing blodiversity. The present sequence represents a novel human arginine-rich protein cDNA. New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and ID NO 215; 51pp; English 2004-238579/22 Disclosure, SEQ 

Sequence 2501 BP; 525 A; 788 C; 728 G; 460 T; 0 U; 0 Other;

Gaps Length 2501; 21; Indels DB 12; 276; Score 1355.4; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 84.0%;
Matches 1562; Conservative ò

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 3443;
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                                                                                                                                                                                                                                                   Human cell cycle-associated cDNA from clone DKFZphtes3_7j3
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.larity 84.0%; Pred. No. 0;
Conservative 0; Mismatches 276;
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in the formation, differentiation and maintenance of multicellular corganisments proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisme. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors are paramaceutical and diagnostic agents, such and receptors of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention proteins, along with the cDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic activities through the stimulation of chondrocytes. The nucleic activities through the tumour in a mammal: In-addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG 706
                                                       invention relates to novel nucleic acids encoding human PRO secreted
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Pred. No. 0;
0; Mismatches 276; Indels 21; G
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2; SEQ ID NO 639; 918pp; English.
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Qy         1307 TGCCTGATACTCCAGGGCAGCCTGTTCCTGCTCCCAAGGAAAGGCATCC         1366           Db         1422 TCCCTGCGAGGCCGAGGCTGCCCCGCTGCTCCCCAAGAAGGCATTC         1472           Qy         1367 TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTCCTCTCCAGAGCCCAGCGAGTCTG         1426           Db         1473 TCAAGAAGTCTCGACAGCGAATCTGGTTACTCCTCTCCCCAGAGCAGTGAATCTG         1532           Qy         1427 GGGAACTCTTAGAACTCCGAGACGAACTGCAGAAGAAGAAGCAGAAAGCTC         1486	Oy 1547 CACAGGCTTCAGGGCTCCTCCACGGCAAGGCCATCTCAAACTCAAATGGCAAGTTCT 1546			OS Homo sapiens. XX XX EN W02004043361-A2. XX PD 27-MAY-2004. XX PF 06-NOV-2003; 2003WO-US035268. XX PR 08-NOV-2002; 2002US-0425235P. XX PA (GETH ) GENENTECH INC.
GCTACGAGTTCCTGGAGACCCTGGGCAAGGCACGGAAGGTGAAGGGGGGGG	462 TCATTGCCATCCATGAAGTGTTTGAGAACAGCAAGATCGTGATGGAGTATG 521 407 CCAGCCGAGGCATCTGTATAATTACATCAGTGAGGCCACGGCTGAGGGGATG 521 407 CCAGCCGAGGCATCTGATAATTACATCAGTGAGGGCCACGGCTGAGTGAG		AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTTAATGGTGAACCCCACCCGTCGGG  [	11242 ATTICITANGAMENTOCOGRANGGANGANIGGUICAAANTCICCAAGGIGGUCGG 1186  11242 ATTICCTCAAGAAGTCCCGCAAGGAGAATGACCCCAGTCTCTCCACAGGIGACCGG 1301  1187 CTGAGGATACCTTCTCGCCCTGGCAAGAGCCTTAAGCTTCCGAAAGGCATTCTCA 1246  11802 CTGATGACACTGCCCTTGCCAGGCAAGAGCTTCCAAGCTTCCGAAAGGCATTCTCA 1361  1247 AGAAAAAGTCCTCTACCTCGTCAGGGGAACAGAGACCCTCAGGAACTCAGACCGG 1306  1247 AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGCCCTCAGGAACTCAGACCGC 1306  1362 AGAAGAAGTCCTCTACCTCTCAGAAAGGGTACAGGAGGACCCTCCGGAACTCAGACCGA 1421

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                                                                                                   Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                    The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogram's syndrome, vasculitis, sarchritis, systemic haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polynucleotide of
               PM;
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7 226 346 TCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATG 406 CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA 106 AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGCACCATCACAAACACAACTGCGGCACC 166 TCATTGCCATCCATGAAGTGTTTGAGAACAGCAAGATCGTGATCGTCATGGAGTTG 521 CCAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCG 526 TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG 586 CTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA 646 CCACTCCCTCGGCCGCAGAGCTAGCCCGGCCGCTGGCGGAAGGGCTGATCAAGTCGCCCA 221 GCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAGGTGAAGAAGAGGCGCGGG 341 AGAGCTCGGGGCCCTGGTGGCCATCAAGTCAATCCGGAAGGACAAAATCAAAGATGAGC 401 AAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCACTCAACCACCCCCCACA 461 ccadocododocorritardaciaciacidededededededededededededededade 581 701 AGCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACCACAAGCACAACCTGCGGCACC 281 GCTACGAGTTCCTGGAGACGCTGGGCCAAGGGCACCTACGGGAAGGTGAAGAGGCACGAG TCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGGATGCCAATGGGAATATCAAGATTG AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA Gaps DB 12; Length 3443; 21; 276; Indels Score 1355.4; Pred. No. 0; 0; Mismatches 71.6%; ilarity 84.0%; Conservative Similarity Best Local Sim Matches 1562; 342 Query Match Best Local S 162 222 47 107 282 227 287 402 347 462 407 522 467 582 527 642 587 702 167

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767	GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCA 826
827	AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCGTCGGG 886
1002	CCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACGGAGTCG 946
947	GGGAACAGGAAGCCCTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCA 1006
1007	
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1187	CTGAGGATACCTCTTCTCGCCCTGGGAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA 1246
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1367	TTAAGAAGTCTCGACAGCGTGAATCTGGTTACTACTCCTCCCAGAGCCCAGCGAGTCTG 1426
1427	GGGAACTCTTAGACGCCAGTGATGTGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC 1486
1487	CACAGGCTTCAGGGCTCCTCCTCCACGCAAGGCATTCTCAAACTCAATGGCAAGTTCT 1546 
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1667	TGTCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA 1726
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Unknown.
Unclassified.
1 (bases 1 to 2902)
Bird,T.A., Virca,G.D., Martin,U. and Anderson,D.M.
Bird,T.A., Virca,G.D., Martin,U. and Anderson,D.M.
Methods for identifying compounds that alter kinase activity
Patent: US 6514719-A 4 04-FEB-2003;
Location/Qualifiers
           AX380972

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Sequence 4 from patent US 6514719.
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121 AAGCAGGGGGCACCATCACAACACAACTGGGGCACCGCTACGAGTTCCTG		735   TCGCCTGGGGTTAGTCTAGTGGGGCCCGGGGGGGGGGGG	975 GTAGCCAGTCATTGGTGGGTTCAACTGGGGTTTACACCACGGAACTGGGGAACCC 1034 961 CTGCGTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGCC

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catalytic domain. Phosphotransferases of the serine or

threonine-specific kinase subfamily. The enzymatic

activity of these protein kinases is controlled by

phosphorylation of specific residues in the activation

segment of the catalytic domain, sometimes combined

reversible conformational changes in the C-terminal

autoregulatory tail."
           LKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARPSRPSGAVSEDS1LSSESFDQLDL
PERLPETPLRGCVSVDNLRGLEQPPSEGLKRWWQESLGDSCFSLTDCQEVTAAYRQAL
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PSDACGLIERGLMYNPTRRATLEDYASHWWYNWGYTTGVGEGEALREGGHPSGDSGRA
SMADWLRRSSRPLLENGAKVGSFFKQHVPGGGSTPVGLERQHSLKKSRKENDMAQNLQ
GDPREDTSSRPGKSLIKLPKGILKKKGSTSSGEVQEDPQELRPVPDTPGQPVPAVSLI
PRKGILKKKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGI
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KAHHKHUNEHRYEPLETLGKGTYGKOKKARRESGRIVALKSIRKUKTROBODLHIR
REIEIMSSLNHPHITALHEVPENSSKIVIWEYASRGDLYDYJSERPELSERDARHF
RQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADPGLSNLYHKGKFLQTFCGSPL
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Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. L., Skalska, U., Sanius, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Ghein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC_clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 40 Row: d Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
Location/Qualifiers
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Submitted (26-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Contact: amg@bcm.tmc.edu
Gunazarne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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/clonce="MGC:30599 IMMOR:3063595"
/tisgue_type="Wammary tumor metastatized to lung.
MMTV-LITE/Wnt1 model. Expression driven by an MMTV-LTR
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Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6"
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/product="1200013B22Rik pr.
/protein_id="AAH33302.1"
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/note="synonym: Snark"
/db_xref="LocusID:74137"
/db_xref="MGI:1921387"
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/strain="Czech II"
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Lukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases I to 2938)

RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altechul, S.F., Zeeberg, B., Buttow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, F.F., Jordan, H., Money, T., Wann, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Scheetz, T.E., Muzny, J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A,
Faley, J., Hellon, E., Ketteman, M., Madan, A.C., Shevchenko, Y.,
Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Blockson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Samilus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,B., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at: http://image.llnl.gov Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.
                                                                                                                                         ROD 04-NOV-2003
clone MGC:61244
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Submitted (13-FB2-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                             BUU46833 2938 bp mRNA linear Mus musculus RIKEN cDNA 1200013B22 gene, mRNA (cDNA 14AGE:6816569), complete cds.
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/srrei="C57BL"6"
/clone="MGC:61244 IMAGE:6816569"
     1941 AGACAAGCCCTAGGAATCTGCTCGAAGCTCAGC 1973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="S_TKC; Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine-specific kinases subfamily. The enzymatic activity of these protein kinases is controlled by phosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal autoregulatory tail"

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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                       /codon_start=1
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1477 CAGAAGICTCCACAGGCTTCAGGGCTCCTCCTCCCACGCAAGGGCATTCTCAAACTCAAT 1536	1537 GGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGAC 1596	1597 CAACTIGGCCTCCTCCCATCCTGCAGCCCGGCCCCGCCCC	1657 GACAGCATCCTGCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAA 1716	1717 ACCCCACTGAGGGCTGTGTGTGTGACAACCTGAGGGGGCTTGAGGAGCCTCCTCA 1776	1777 GAAGGICTGAAGCGATGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAGAC 1836 	1837 TGCCAAGAGGTGACTGCAGCCTACAGACCTAGGAATCTGCTCAAAGCTCAGC 1893 	om Paten		Muticae) Muticae	Ampk-rela Patent: W 1149336 C	μ	<pre>y Match Local Similarity 93.4%; Score 1683.4; DB 6; Length 2026; hea 1769. Conservative 0. Mismarches 121, Indele 2.</pre>	GGTGGCCTTACTCCAGGCCCGAGCTCCTCCTCGCCTCGC	TCGGAGAGCCCCGGCCGCTGGCGGAGCCTCATCAAGTCGCCTAAACCTCTCATGATGAAG	**Accorded Control of the Control of	155 AAGCAGGCAAGCGGCACCTACAAACACAACCIGAGGGACCGGTACGGAGTICCIG 254 181 GAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGCACGAGAGAGCTCGGGGCGT 240 181 GAGACCCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAAGCACGAGAGAGCTCGGGACGC 314

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	121 AAGCAGGCGGTGAAGCGGCACCATCACAAACACAACCTGGGGCACCGCTACGAGTTCCTG 180	181 GAGACGCTGGGCAAGGCACCTACGGGAAGGTGAAGAAGGCACGAGAGACTCGGGGCGT 240 	241 CTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGGATCTGCTGCAC 300 	301 ATACGGAGGAGATCATGACTTCACTCAACCACCCCCACATCATTGCCATCAT 360 	361 GAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGCCAGCCGAGGGGAT 420	421 CTGTATGATTACATCAGTGAGCGGCCACGGCTGAGTGAGCGGGACGCCAGGCATTTCTTC 480 	481 CGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTC 540	541 AAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTC 600 	601 TCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTCTAGGC 660	661 TCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTCTG 720 	721 GGCGTTCTCCTGTACATCCTGGTGCCATGCCATGCCCTTTGACGGGCAGGATCATAAA 780	781 ACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATGCC 840	841 IGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCCGTCGGGCCACACTGGAGGAT 900	901 GTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACCGGGGTTGGGGAGTCGGGGAAGCC 960 	961 CTGCGTGAGGGTGCCCTAGTGGTGACTTTGGCCGGCCTCCATGGCGGACTGGTTA 1020	1021 CGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGCAG 1080	1081 CACGTGCCGGGAGGTGCAACTGTACCTGGGCTGGAGCGGCAACATTCTCTTAAGAAG 1140	
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1223 TCCCGCAAGGAGAATGACATGGCTCAGACTCTGCAGAATGACCCCAGTTGAAGATACTTCC 1282
                                                                         GGGCAGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGA 1380
                                                                                                                                                                                                                                                                       CAGCGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGAC 1440
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus (Norway rat)
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On Nov 15, 2002 this sequence version replaced gi:23269681.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/xat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the serimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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Direct Submission
Submitted (O2-UUL-2002) Human Genome Sequencing Center, Department
Submitted (O2-UUL-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 291762)
Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                           Assembly program: Phrap; version 0.990329
Consensus quality: 226653 bases at least Q40
Consensus quality: 230853 bases at least Q30
Estimated insert size: 233445; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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5 284658: contig of $834 bp in length
284758: gap of unknown length
9 287234: contig of 2476 bp in length
287334: gap of unknown length
5 297762: contig of 4428 bp in length
Location/Qualifiers
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of 1405 bp in length
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274631: gap of unknown length
276287: contig of 1656 bp in length
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|organism="Rattus norvegicus"
|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-27433"
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99.3%; Pred. No. 0;
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0; Mismatches
                  Center project name: GWLD
Center clone name: CH230-274J3
Project Information
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/note="wgs_contig"
95132. .96554
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
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                 CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTA
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3700, a novel human protein kinase and
Patent: WO 0224921-A 1 28-MAR-2002;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Pred. No. 0;
0; Mismatches

    .3353
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 1 from Patent |
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	d 10 d	AUTHORS TITLE JOURNAL COMMENT	FEATURES	ORIGIN  ORIGIN  1486  Query Match  Local Similarity 84.1%; Pred. No. 0;  Best Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservative 0; Mismatches 275; Indels 21; Gaps 2;  Local Similarity 84.1%; Pred. No. 0;  Matches 1563; Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Conservation of Nicolar Similarity Con
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	AKO74830  Homo sapiens cDNA FLJ90349 fis, clone NT2RP2003179, weakly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1).  AKO74830.1 G1:22760531  Oligo capping; fis (full insert sequence).  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Homo sapiens (human)  Ametaca, Macazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  Bukaryota; Macazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  Sugiyama, T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,  Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,  Kayina,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,  Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and  Ninomiya,K.
	RESULT 14 AK074830 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL COMMENT COMMENT
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GCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTACACAGGGCCCAGAGGTGG
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                                                                                                                                                                                                                                                           'note="unnamed protein product"
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xref="taxon:9606"
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Best Local Similarity 84.1%;
Matches 1563; Conservative
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Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Rlausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, N.K.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morkernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and intital analysis of more than 15,000 full-length
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Web site: http://www.nisc.nih.gov/
Contact: nisc mg/eahgai.nih.gov
Contact: nisc mg/eahgai.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Waker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                               1883 GAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGACAG 1942
                                                                                                                                                                                                                                                                                                                                                                                 BC017306 3402 bp mRNA linear PRI 29-JUN-2004 Homo sapiens likely ortholog of rat SNF1/AMP-activated protein kinase, mRNA (cDNA clone MGC:29812 IMAGE:5088037), complete cds.
1835 ACTGCCAAGAGGTGACTGCCGACCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 1893
                                                                                                                                                                                                         1943 ACTGCCAGGAGGTGACGACCTACCGACAGGACTGAGGTCTGCTCAAAGCTCACC 2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3402)
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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On Aug 19, 2003 this sequence version replaced gi:16878205.
Contact: MGC help desk
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Homo sapiens
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                                                       1781
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AUTHORS
TITLE
JOURNAL
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BC017306
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KEYWORDS
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IMSSLNHPHIIAHHEVFENSSKIVIVMEYASRGDLYDYISERQQLSEREARHFFRQIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQĞKFLQTFCGSPLYÄSP
EIVNGKPYTGPEVDSWSLGVLLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDA
CGLIRWLLMVNPTRRATLEDVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WLRRSSRPLLENGAKVCSPFKQHAPGGGSTTPGLERQHSLKKGRKENDMAQSLHSDTA
DDTAHRPGKSULKLPKGILKKKVSASAEGYQEDPPELLSPTPASPGQAPLLPFKKGILK
KPRQFSGGYYSSPEPSEGGELLDAGDVVSGDPKGQKPPQASGLLLHRKGILKLNGKF
SQTALELAAPTTFGSLDELAPPRPLARASRPSGAVSEDSILSSESPOOLDLPERLPEP
PLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPLGDSCFSLTDCQEVTATYRQALRVC
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: o Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13569921.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCCGCCCTGGCCTCGGAGAGCGCCCGGCTGGCGGACGGGCTCATCAAGTCGCCTA 106
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494 CCAG	467 CCAGG         554 CTAGG	527 TTCA(      614 TCCA(	587 CTGA(      674 CTGA	647 GCCC         734 GCCC	707 ACAGO      794 ACAGO	767 GGCAC      854 GGCAC	827 AGCC 	887 CCAC	947 GGGAJ      1034 GAGAC	1007 TGGC       194 TGGC	1067 GCTT(      1154 GCTT(	1127 ATTC       214 ATTC	1187 CTGA(       274 CTGA:	1247 AGAAJ      1334 AGAA	1307 TGCC           1394 TCCC	1367 TTAAC 	1427 GGGAJ       1505 GGGAK	1487 CACA(

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GAGAGATTGAGATCATGTCATCCCTCAACCATCCTCATATCATCAGTATTTATGAAGTGT 367

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PRIOR APPLICATION NUMBER: 60/469,014
PRIOR FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 239
SOFTWARE: PATENTIN VERSION 3.2
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Score 493.6;
Pred. No. 1.10
26.1%;
66.6%;
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US-101-36
Sequence 36, Application US/10840512
GENERAL INFORMATION:
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: GRACKICK, GLEN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILING DATE: 2004-05-07

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APPLICANT: Miller, Barbara

APPLICANT: Miller, Barbara

APPLICANT: Gachotte, Daniel

APPLICANT: Gachotte, Daniel

APPLICANT: Baddy, Avutu

APPLICANT: Reddy, Avutu

APPLICANT: Crosley, Rodney

TITLE OF INVENTION: Nucleic Acid Compositions Conferring Altered Metabolic Characterie

FILE REFERENCE: DOW-08552

CURRENT PAPLICANT: 2004-02-26

NUMBER OF SEQ ID NOS: 7560

SOFTWARE: Patentin version 3.1

SEQ ID NO 6208

LENGTH: 944
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                                                        107 AACCTCTGATGAAGAAGCAGGGGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACC
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11.7%; Score 221; DB 7; L
Best Local Similarity 56.2%; Pred. No. 1.1e-38;
Matches 457; Conservative 0; Mismatches 350;
     Mismatches
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Matches 429; Conservative
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                            AGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCT
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APPLICANT: CHAN, LINGGRAND JAIME
APPLICANT: CARCALA, PABLO DOMINGUEZ
APPLICANT: HANGEN, HONDA
APPLICANT: HANGEN, HONDA
APPLICANT: KAUFMANN, JOERG
APPLICANT: KAUFMANN, JOERG
APPLICANT: KANDAZZO, FILIPO
APPLICANT: MOLER, EDWARD J.
APPLICANT: REINHARD, CHRISTOPH
APPLICANT: REINHARD, CHRISTOPH
APPLICANT: REINHARD, CHRISTOPH
APPLICANT: SUDDUTH-KLINGER, JULIE
TITLE OF INVENTION: IN CANDER: JO616, 900
FILE REFERENCE: 2300-21987
CURRENT APPLICATION NUMBER: 10/616, 900
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2001-06-01
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 2001-02-11
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PRIOR PILING DATE: 2003-04-04
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89.9%; Pred. No. 1.2e-77;
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Best Local Similarity
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Gaps

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Length 4094; Indels

Score 197.4; DB 1; Pred. No. 1.9e-33; 0; Mismatches 341;

10.4%; 54.7%;

Conservative

Matches 415; 168

Query Match

Similarity

227 217 287 277

CTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAGA craccadearcearcearcearcearadeacaacircearcearcadeacaeaca 228 GAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCA ccrccrccaaggccaaggrrgcrarraaaircaragaraaggccagcrggarga 347

GGATCTGCTGCACATACGGAGGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACAT

218 288 278 AAACTTGAAGAATTTTCCGGGAGGTTCAGATAATGAAGATGCTTTGCCATCCACAT CATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGC CATCAGACTCTACCAGGTCATGGAGACAGAGGCGCATGATTTACCTGGTGACAGAATACGC 

348 338 408 398 468 458 528 518 588 578 648

CAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACCAGAACGGGATCGT rceacegaagricaaacaearceacaecegrerarrirrercacrercegaararer TCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGC TCATCGTGATTTAAAAGCCGAAACTTACTTCTGGACGCCAATCTGAATATCAAATAGC TGACTITIGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGAG AGACTITGGCTICAGCAACCTCTTCACTCCAGGGCAGCTGCTGAAGACGTGTGTGCTGTGCCG CCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGGCCCAGAGGTGGA 

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                                                GGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAAATCAAAGATGAGCAGGATCT 293
                                                                                                           GCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCCACATTGTTGC 353
                                                                                                                                         239 AGAGAAAGTTCGCAGAGAGATTAAAATCCTGAGGTTGTTTATGCATCCACACATCATAAG 298
                                                                                                                                                                     CATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGCCAGCCG 413
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                                                                                                                                                                                                                                                                                                                  768 GCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCCAA
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FILE REFERENCE: 034536-1455
CURRENT APPLICATION NUMBER: US/10/840,512
CURRENT FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: 60/469,014
PRIOR FILING DATE: 2003-05-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 37, Application US/10840512; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: CAENEPEEL, SEAN
APPLICANT: MANNING, GERARD
PPLICANT: CHARYDCZAK, GLEN
APPLICANT: GRIGORIEV, IGOR
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US-10-840-512-37
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APPLICANT: SUGEN, INC.
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CAENEPEEL, SEAN
APPLICANT: CHANYDCZAK, GLEN
APPLICANT: CHANYDCZAK, GLEN
APPLICANT: GRIGORIEV, IGOR
TITLE OF INVENTION: NOVEL KINASES
FILE REFERRNCE: 034536-1454
CURRENT APPLICATION NUMBER: PCT/USO4/14421
CURRENT APPLICATION NUMBER: 60/469,014
PRIOR PRIOR PLING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 239
SEQ ID NO 37

TYPE: DNA ORGANISM: Mus musculus

LENGTH: 4094

Sequence 37, Application PC/TUS0414421 GENERAL INFORMATION:

PCT-US04-14421-37

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                                                                                                                                                                                               GGATCTGCTGCACATACGGAGAGATTGAGATCATGTCTTCACTCAACCACCCCCACAT 347
                                                                                                                                                                                                              278 AAACTIGAAGAAGATITICCGGGAGGITCAGAIAATGAAGAIGCTITGCCATCCACCACAT 337
                                                                                                                                                                                                                                      CATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTATGC 407
                                                                                                                                                                                                                                                 TCACCGAGATCTCAAGCTGGAAACATCCTTCTAGATGCAATGGAAACATCAAGATTGC 587
                                                                                                                                                                                                                                                                                                                                                                       588 TGACTITIGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGAG 647
                                                                                                                                                                                                                                                                                                                                                                                                            CCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCCAGAGGTGGA 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACGG 767
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                                                                                                                                                                                                                                                                                                                     468 CAGGCATTTCTTCCGACAGATCGTGTCTGCCCTGCACTACTGCCACAGAACGGGATCGT 527
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                                                                                                                    CTACGAGTTCCTGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAGA
                                                                              Length 4094;
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                                                                              Query Match 10.4%; Score 197.4; DB 7; Best Local Similarity 54.7%; Pred. No. 1.9e-33; Matches 415; Conservative 0; Mismatches 341;
; NUMBER OF SEQ ID NOS: 239; SOFTWARE: Patentin version 3; SEQ ID NO 37; LENGTH: 4094; TYPE: DNA TYPE: DNA CONSENS: NOS-10-840-512-37
                                                                                                                     168
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134 AGCGGCACCATCACAAACAACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCA 193
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                                                         Repression
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APPLICANT: Helentjalls, .....
APPLICANT: Macool, Daniel
APPLICANT: Maco, Guo-Hua
APPLICANT: Maco, Guo-Hua
TILE OF INVENTION: Plant Carbon Catabolite Rep
FILE REFERENCE: BB-1315
CURRENT APPLICATION NUMBER: US/10/998.525
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: US/09/857,522
PRIOR APPLICATION NUMBER: PCT/US99/29824
PRIOR PILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 2107
                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Zea mays
US-10-998-525-5
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RESULT 7
US-10-998-525-5
i Sequence 5, Application US/10998525
i GENERAL INFORMATION:
APPLICANT: Allen, Stephen
APPLICANT: Allen, Stephen
APPLICANT: Sakai, Hajime
APPLICANT: Weng, Zude

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TYPE: DNA
CORGANISM: Oryza sativa
US-60-638-099-214
                                                                                                                                                                                                                                          Best Local Similarity
Matches 363; Conserv
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US-10-998-525-21
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                                                                                                                                                                                                                                                                                                                                                                                                               CAACCCTTTGGGCGGTTACCGAATTGGCAAAACCCTAGGAATTGGGTCGTTCGGTAAAGT 83
                                                                                                                                                                      APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic Phenotypes
FILE REFERENCE: 38-21(53720)
CURRENT APPLICATION NUMBER: US/60/638,099
CURRENT APPLICADION NUMBER: US/60/638,099
NUMBER OF SEQ ID NOS: 48056
SEQ ID NO 231
                    TITATGCTCTTCTTGTGGCACTCTCCCATTTGACGATGAGAATATTCCAAACCTTTTCA
TGTACATCCTGGTGCATGCCATGCCCTTTGACGGGCAGGATCATAAAACACTGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTCAACCACCACCACATGATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGT
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                                                                                                                                                                                                                                                                                                                                     Length 1512;
                                                                                                                                                                                                                                                                                                                                 Score 186; DB 9; Length 15
Pred. No. 4.6e-31;
0; Mismatches 280; Indels
                                                                                                                                             Sequence 231, Application US/60638099 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 tch 9.8%; al Similarity 56.5%; 367; Conservative C
                                                    AGCAAATCA 799
                                                                            AGAAAATAA 902
                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Zea mays
US-60-638-099-231
                                                                                                                    RESULT 8
US-60-638-099-231
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Best Local 8
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                                     625 ACCCTTCCATTTGATGACGAGAATATTCCCAACCTTTTAAGAAATAA 673
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Sequence 214, Application US/60638099; GENERAL INFORMATION:
    APPLICANT: Edgerton, Michael D
    TITLE OF INVENTION: Transgenic Plants with Enhanced Agronomic FILE REFERENCE: 38-21(53720)
    CURRENT APPLICATION NUMBER: US/60/638,099
    CURRENT FILING DATE: 2004-12-21
    NUMBER OF SEQ ID NOS: 48056
    SEQ ID NO 214
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APPLICANT: Allen, Stephen
APPLICANT: Heppard, Elmer
APPLICANT: Sakai, Hajime
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      APPLICANT: Helentjaris, Tim
APPLICANT: Macool, Daniel
APPLICANT: Macool, Daniel
APPLICANT: Macool, Daniel
TILE APPLICANT: Macool, Daniel
TILE OF INVENTION: Plant Carbon Catabolite Repression Proteins
FILE REFERENCE: BB-1315
CURRENT APPLICATION NUMBER: US/10/998,525
CURRENT FILING DATE: 2004-11-29
PRIOR APPLICATION NUMBER: US/09/857,522
PRIOR APPLICATION NUMBER: PCT/US99/29824
PRIOR PILING DATE: 1999-12-15
PRIOR PELING DATE: 1999-12-15
PRIOR PILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 21
SEQ ID NO 21
SEQ ID NO 21
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                                                                                                                                                                                                                                                                                                                                                                   Length 2006;
                                                                                                                                                                                                                                                                                                                                                               Score 179.6; DB 7; Length
Pred. No. 1.2e-29;
0; Mismatches 284; Indels
                                                                                                                                                                                                                                                                                                                                                                   9.5%;
Weng, Zude
Helentjaris, Tim
Macool, Daniel
                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Triticum aestivum
US-10-998-525-21
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.8
Matches 363; Conservative
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RESULT 11 US-10-995-561-364

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1112
Sequence 364, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPRENCE: CLOOLSS9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 364
LENGTH: 3394
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Pred. No. 1.5e-29;
1; Mismatches 352;
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Best Local Similarity 53.1%;
Matches 403; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-364
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                           Sequence 361, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (PINTENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 87702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 361
LENGTH: 3442
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Pred. No. 1.5e-29;
1; Mismatches 352;
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Best Local Similarity 53.1%;
Matches 403; Conservative
                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-361
RESULT 12
US-10-995-561-361
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                                                                                                                                                      Sequence 363, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS C
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPRENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 363
LENGTH: 3466
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53.1%; Pred. No. 1.5e-29;
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                                                                                                                                  Sequence 359, Application US/10995561
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: CENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRAESEQ for Windows Version 4.0
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Pred. No. 1.5e-29;
1; Mismatches 352;
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Matches 403; Conservative
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ORGANISM: Homo sapiens
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US-10-995-561-359
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LENGTH: 3487
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS AND DRUG RESPONSE, METHODS C
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE REFERENCE: CLOUSES9
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 3514
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1; Mismatches 352;
                                                                                                                                                                                                                                                 885 GGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAA
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Search completed: January 25, 2005, 07:13:05 Job time : 357.728 secs

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241 AGAAGCAGCGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACCGCTACGAGTTCC
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Best Local Similarity 100.
Matches 2902; Conservative
ORGANISM: Mus musculus
US-09-579-664B-4
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Sequence 16539, A
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US-09-270-767-16539
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US-08-557-006C-34
US-08-557-006C-34
US-08-557-006C-38
US-08-557-006C-38
US-08-557-006C-38
US-09-744-528-112
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ALIGNMENTS

61 CCGCGGGCTCAGCGCGCGCTACTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCCGCA 120 AGAAGCAGGCGGTGAAGCGGCACCATCACAAACACCTGCGGCACCGCTACGAGTTCC 300 1 CACTAGTGGATCCAAAGAATTCGGCACGAGGCGTGCTCGGGTGCGGGTGTGACCTCTGAG 121 CCATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGCCAGGCTCCCTCGGCCTCCGCCTGG 181 CCTCGGAGAGCGCCCCGCTGGCGGACGGGCTCATCAAGTCGCCTAAACCTCTGATGA 61 CCCGCGCCTCAGCGCGCGCTACTGCTGCCCGACCCCACTCCACCTCGCGGTCCCCGCA CCTCGGAGAGCGCCCGGCCGCTGGCGGACGGGCTCATCAAGTCGCCTAAAACCTCTGATGA ö Length 2902; CACTAGTGGATCCAAAGAATTCGGCACGAGGCGTGCTCGGGTGCGGCTG Indels US-09-579-664B-4

US-09-579-664B-4

Sequence 4, Application US/09579664B

Patent No. 6514719

GENERAL INFORMATION:

APPLICANT: Immunex Corporation

APPLICANT: Wirca, G. Duke

APPLICANT: Wirca, G. Duke

APPLICANT: Martin, Unia

APPLICANT: Martin, Unia

APPLICANT: Martin, Unia

APPLICANT: Wirca, G. Duke

FILE REPRENCE: 2923-4

CURRENT APPLICATION NUMBER: US/09/579,664B

CURRENT FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 2902 DB 4; ; Score 2902; I; Pred. No. 0; 0; Mismatches 100.0%;

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                                                                                                                                                                            Score 202.6; DB
Pred. No. 4e-42;
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001306
CURRENT APPLICATION NUMBER: US/09/984,890
CURRENT FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PASLESQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2175
                                                                                                                                                                           Query Match 7.0%;
Best Local Similarity 54.9%;
Matches 422; Conservative
                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-890-1
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RESULT 5 US-10-274-194-1 'S Gequence 1, Application US/10274194 'Patent No. 6706511

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APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: SCLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND ITILE OF INVENTION: THEREOF FILE REFERENCE: CL001306DIV
CURRENT PPLLICATION NUMBER: US/10/274,194
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       576 AGACTITIGGCTTCAGCAATGAATTCACCTTTGGGAACAAGCTGGACACCTTCTGTGGCAG
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ORGANISM: Homo sapiens
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rcrareccreecegaarrer 1
              64.3%;
Query Match
Best Local Similarity 64.39
Matches 284; Conservative
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, LOCATION: (106)..(2112)
US-09-930-181-1
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LENGTH: 2908
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                                                                               Sequence 1257, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPRENCE: File Reference: 7326.094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION DAIE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1257
LENGTH: 484
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburse et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62217
SOFTWARE: PatentIn Ver. 2.0
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US-09-270-767-1257
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; ORGANISM: Drosophila melanogaster
US-09-270-767-16539
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US-09-270-767-16539/c
                                                 US-09-270-767-1257/c
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LENGTH: 484
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Patent No. 6455292
GENERAL INFORMATION:
APPLICANT: OriGene Technologies
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 16U 101 V1
CURRENT APPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                    TGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACATCATTG 474
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Best Local Similarity 53.5%; Pred. No. 7.2e-38;
Matches 413; Conservative 0; Mismatches 356;
Score 189.2; DB 4;
Pred. No. 5.2e-39;
0; Mismatches 158;
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Sequence 39, Application US/08557006C

Rater No. 625847

GENERAL INFORMATION:
APPLICANT: Bari, Rajindar K.
APPLICANT: Carling, David

APPLICANT: Forder, Nobert A.
ITILE OF INVENTION: NUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE
FILE REFERENCE: NGAP/PHM37588/UST
CURRENT APPLICATION NUMBER: US/08/557,006C

CURRENT FILING DATE: 1996-03-06

PRIOR FILING DATE: 1994-05-20

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

SEXION SEQIENCE: Patentin Ver. 2.1

SEQIENCE: Patentin Ver. 2.1

FEMALEY. SEGIENCE: Patentin Ver. 2.1
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ATCATTGCCATCCATGAAGTGTTTGAGAATAGCAGCAAGATTGTGATTGTCATGGAGTAT 527
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                                                                337 grectaaagergeacgacgrrrangaaacaaaaararrreracerggrecragaacae 396
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NAME/KEX: gene
LOCATION: (1)..(1747)
OTHER INFORMATION: Full length cDNA sequence fragment of Human AMPK
OTHER INFORMATION: fragment begins at nucleotide 24 and ends with
JOTHER INFORMATION: nucleotide 1765
US-08-557-006C-39
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ORGANISM: Rat
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Patent No. 6258547
GENERAL INFORMATION:
APPLICANT: Beri, Padindar K.
APPLICANT: Carling, David
APPLICANT: Forder, Robert A.
TITLE OF INVENTION: WUCLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE; FILE REFERENCE: WGAPPHATSP88/UST; CURRENT APPLICATION NUMBER: US/08/557,006C
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Score 182.4; DB 3;
Pred. No. 7.4e-37;
0; Mismatches 381;
        6.3%;
                                             al Similarity 53.0
437; Conservative
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        Query Match
Best Local S:
Matches 437
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GENERAL INCOMENTATION:

APPLICANT: Beri, Rajindar K.

APPLICANT: Carling, David

APPLICANT: Carling, David

APPLICANT: Porder, Robert

TILE OF INVENTION: WULLEIC ACID ENCODING AMP-ACTIVATED PROTEIN KINASE

FILE REFERENCE: NGAP/PHM37588/UST

CURRENT APPLICATION NUMBER: US/08/557,006C

CURRENT FILING DATE: 1996-03-06

PRIOR APPLICATION NUMBER: PCT/GB94/01093

PRIOR APPLICATION NUMBER: GB 9310489.1

PRIOR PLILNG DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

PRIOR FILING DATE: 1993-05-21

SOFTWARE: PACHICATION NUMBER: GB 9318010.7

SOFTWARE: PACHICATION NUMBER: GB 9318010.7

SOFTWARE: PACHICATION NUMBER: GB 9318010.7

SOFTWARE: PACHICATION NUMBER: GB 9318010.7

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Best Local Similarity 53.1%; Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                           ; Sequence 38, Application US/08557006C; Patent No. 6258547; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human AMP protein kinase
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CURRENT FILING DATE: 1996-03-06
PRIOR APPLICATION NUMBER: PCT/GB94/01093
PRIOR FILING DATE: 1994-05-20
PRIOR APPLICATION NUMBER: GB 9310489.1
PRIOR FILING DATE: 1993-05-21
PRIOR FILING DATE: 1993-05-21
PRIOR PILING DATE: 1993-08-31
PRIOR FILING DATE: 1993-08-31
SOFTWARE: PATENT NUMBER: GB 9318010.7
SOFTWARE: PATENT NOS: 44
SOFTWARE: PATENT NOS: 44
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                             350 GAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCA 409
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TITLE OF INVENTION: No. 6743619el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
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CURRENT APPLICATION NUMBER: US/09/774,528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 112, Application US/09774528
Patent No. 6743619
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
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Zhao, Qing A.
Yang, Yonghong
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Wang, Dunrui
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Xue, Aidong J
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CGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACGGGCAGGATCATAAAAC 904
                                                                                                                          TGTTATCCTGTATGCCCTTCTCTGTGGCACCCTCCCGTTCGACGATGAGCACGTGCCTAC 662
                                                                                                                                                                                                                                                                                                                  TGCCACTCTGCTGATGCACATGCTGCAGGTGGACCCCTTGAAGCGAGCAACTATCAAAGA 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08677298
Patent No. 5863729
GENERAL NO. POWALTON:
APPLICANT: Piwnica-Worms, Helen
TITLE OF INVENTION: NIASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/677,298
FILING DATE: 09-JUL-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: CATUCHERS, Jennie M.

REGISTRATION NUMBER: 9-96
TELEPHONE: (303) 499-8089
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                               1022 TGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCA 1059
                                                                                                                                                                                                                                                                                                                                                                                                              783 CATACGAGAGCATGAATGGTTTAAACAGGATTTGCCCCA 820
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Pred. No. 3.5e-36;
0; Mismatches 352;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ilarity 53.2%;
Conservative
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Best Local Similarity
Matches 404; Conserva
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STRANDEDNESS:
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LOCATION:
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                    US-09-930-181-3
; Sequence 3, Application US/09930181
; Sequence 3, Application US/09930181
; Patent No. 645529.
; GENERAL INFORMATION:
; APPLICANT: Oxidene Technologies
; TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brai; FILE REFERENCE: 16U 101 V1
; CURRENT APPLICATION UNDERR: US/09/930,181
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 3364
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                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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; LOCATION: (48:
US-09-930-181-3
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Pred. No. 2.7e-35;
0; Mismatches 371; Indels
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL_Genes Version 2.0
SEQ ID NO 112
LENGTH: 2899
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 52.4%;
Matches 412; Conservative
                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (119)..(2899)
US-09-774-528-112
                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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1001 CCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACA 1056
                                       1000 ACGCCCCCCACGCTAGAGCACATTCAGAAACACATATGGTATATAGGGGGCAAGA 1055
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                                                                                                                                                                                                                        APPLICANT: Rory A.J. Curtis
TITLE OF INVENTION: 55053, A No. 6787345el Human Bukaryotic Kinase
TITLE OF INVENTION: and Uses Therefor
FILE REFERENCE: MN. - 206
CURRENT APPLICATION NUMBER: US/10/003,690
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/248,893
PRIOR PILING DATE: 2000-11-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FASESEQ for Windows Version 4.0
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1.8e-34;
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52.7%; Pred. No. 1.8e-34;
live 0; Mismatches 355; Indels
                                                                                                                                                        Sequence 3, Application US/10003690 Patent No. 6787345 GENERAL INFORMATION:
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Matches 399, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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US-10-003-690-3
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LENGTH: 2334
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Search completed: January 25, 2005, 01:59:42 Job time : 241.428 secs

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January 24, 2005, 20:17:54; Search time 1516.67 Seconds (without alignments) 10994.228 Million cell updates/sec
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'/ cgnz 6/ptodata/2/pubpna/USO6 NEW PUB. seq:*
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GenCore version 5.1.6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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2902
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Perfect score:
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Maximum DB 8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	4, Appli	22, Appl	1, Appli	87, Appl	21, Appl	27, Appl	, Appli	43, Appl	25, Appl	639, App	11, Appl	215, App
Description	Sequence 4, Appli	Sequence	Sequence	Sequence	Sequence	Sequence 27, Appl	Sequence 1, Appli	Sequence	Sequence	Sequence	Sequence	Sequence 215, App
SUMMARIES	US-10-355-975-4	US-10-322-281-22	US-10-343-514-1	US-10-343-514-87	US-10-322-281-21	US-10-343-514-27	JS-09-963-159-1	US-10-423-543-43	US-10-322-281-25	US-10-370-715B-639	US-10-618-941-11	US-10-302-172-215
1 B0	15	11	17	17	11	17	9	16	17	18	18	16
% Query Match Length DB	2902	3073	2929	2027	37278	2026	3353	3353	3404	3443	3463	2501
% Query Match	100.0	98.7	71.2	69.7	8.99	61.0	47.5	47.5	47.4	47.4	47.4	47.3
Score	2902	2863.4	2066.8	2022.2	1938.8	1771.4	1379	1379	1375.8	1374.2	1374.2	1372.2
Result No.	1	1	m	4	c)	9	7	80	σ	10	11	12

Sequence 38, Appl Sequence 3, Appli Sequence 45, Appl Sequence 13, Appl Sequence 70, Appl Sequence 70, Appl	*********	Sequence 95, Appl Sequence 96, Appl Sequence 94, Appl Sequence 15, Appl Sequence 1, Appl Sequence 1541, Appl Sequence 1541, Appl Sequence 1541, Appl	0 P P B B B B B B B B B B B B B B B B B
034-3 594-3 514-1 514-7	US-10-382-829 US-10-343-514 US-10-343-514 US-10-343-514 US-10-343-514 US-10-343-514 US-10-343-514	-10-343-514-95 -10-343-514-96 -10-343-514-94 -10-343-514-35 -780-949-1 -10-354-358-81 -10-342-887-15	18 US-10-723-860-2552 18 US-10-723-860-6703 9 US-09-780-949-3 9 US-09-780-949-5 17 US-10-343-514-34 17 US-10-343-514-34 17 US-10-343-514-10 17 US-10-343-514-10 17 US-10-343-514-10 17 US-10-343-514-10 17 US-10-343-514-10
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1370.6 1360.2 1360.2 1071.4 943.4 849.2	649.2 648.2 648.2 648.2 643.2 583.2	534 515 513 511.6 507.6 507.6 507.6	507.6 506.4 506.4 506.4 493.6 474.6 383.4 381.4 55.6
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## ALIGNMENTS

ö 120 61 CCCGCGGCTCAGCGCGCGCTGCTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCA 120 9 9 1 CACTAGTGGATCCAAAGAATTCGGCACGAGGCGTGCTCGGGTGCGGCTGTGACCTCTGAG 1 cactagracicaaagaatrcggcacgaggcgrgcrcgggrgcggcrgrgagg 61 ccceceecrcaececececracracracrecceacccarcrecacrecececa 0; Gaps DB 15; Length 2902; Indels APPLICANT: Immunex Corporation
APPLICANT: Bird, Timethy A.
APPLICANT: Bird, Timethy A.
APPLICANT: Virca, G. Duke
APPLICANT: Virca, G. Duke
TITLE REPERENCE: 2923-A
CURRENT APPLICATION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-A
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US/10/355,975
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 2902
TYPE: DNA
CREATER HOS musculus
COSTANTS NO MUSE MUSCUlus
COSTANTS NO MUSE MUSCUlus
COSTANTS NO MUSE MUSCUlus
COSTANTS NO MUSE MUSCUlus ö Query Match
100.0%; Score 2902; Sest Local Similarity 100.0%; Pred. No. 0; Matches 2902; Conservative 0; Mismatches ; Sequence 4, Application US/10355975; Publication No. US20030162277A1; GENERAL INFORMATION: US-10-355-975-4 엄 QC ઠે ઠે

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1201 AGCACGTGCCGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAACATTCTTTAAGA 1260	141   CAGGGCAGCTGTCCTGCTGCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTC   1500	1621   GGCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCCT	10   10   10   10   10   10   10   10	204 204 210 210	2101 GAGTACATCAAGGGCTCTACGTCTGACTGAACCTGAAGGTGAGAAATCGC 2160 2101 GAGTACATCAAGGGCTCTACGTCTGCACTGAACCTGAACGTGAAAGATGAGAAATCGC 2160 2101 GAGTACATCAAGGGCTCTACCTGCTGCTGACTGAACCTGAAAGATGAGAAAATCGC 2160 2161 ATTGATGTGGAAAGGAATGGGAACCCTTGCTGCCCGAGTGTTATAGTGGGGTGGCTGAA 2220 2161 ATTGATGTGGAAAGGAATGGGAACCCTTGCTGCCCGAGTGTTATAGTGGGGTGGCTGAA 2220 2221 GGTGCCTACCTTGTGCCATGAGTGTCACCCATGATTCCCACCTGTTCTCTGG 2280 2221 GGTGCCTACCTCTTGTGCCATGAGTGTCACCCATGACTTTCCCACCTGTTCTCTGG 2280 2221 GGTGCCTACCTCTTGTGCCATGAGTGTCACCCATGACTTTCCCACCTTGTGG 2280 2221 GGTGCCTACCTTTGTGCCATGAGTGTCACCATGAGTTTCCCACCTTGTTCTGTG 2280
6 6 6 6 6 6 6	8 6 8 6 8	8 8 8 8 8	3 6 8 6 8 6 8	8 8 8	3 4 3 4 3 4 3
121   CCATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGCTCCCTCGGCTCCGCCTGG	GTCTGGTGGCCATCAGGTAGGAAAGACAAAATGAAGAGGGGGGAGGTCTGCTGCGGGGGGGG		661 TCAAGCTGGAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTGCTCACTTTGGCC 7 721 TCTCCAACCTGTACCACAGGCAAGTTCCTCCAAGACTTGTGGGAGCCCTTTTGGCC 7 721 TCTCCAACCTGTACCACAAGGCAAGTTCCTCCAAGACGTTCTGTGGGAGCCCTCTTTACG 7 721 TCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTTACG 7 781 CCTCGCCTGAAATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGGACGCTGCTTC 8 781 CCTCGCCTGAAATAGTCAACGGGAAGCCCTATGTGGGGCCCAGAGGTGGACGCTGGTCTC 8 841 TGGGCGTTCTCCTGTACATCCTGGTGCACGCCCAGAGGATCATA 9	1	1021   ATGTAGCCAGTCATTGGGGGTCACCCGGAGTCGGGGAACAGACAGAACAAACAAAACAAAACAAAAACAAAAAA

61 CCGACCCACTCCACCTCGCGCACCATGGAGTCGGTGGCCTTACTCCAGCGCCC 120  152 GAGCCAGGCTCCCTCGGCCTCGGCCTCGGAGAGCGCCCGGCCGCAGCGGACGC 211  [121 GAGCCAGGCTCCCTCGGCCTCGGCCTCGGAGAGCGCCCGGCCGG	CAAAATCAAAGATGAGGATCTGCTGCACATTGGGAGGAGATTGAGATCATGTTCTTC  [		1   1   1   1   1   1   1   1   1   1	GAACCCCACCGGGCCACCACTGGAGGATGTAGCCGGTCATTGGTGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGGGGTCAACTGGTGGTCAACTGGTGGGGGTCAACTGGTGGGGGTCAACTGGTGGGGGTCAACTGGTGGTGATTACACCACCGGGTCAGGGGTCAACTGGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGGGGGGCCCCCCTAGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGTGAACTGGTGGGGGGGG
8 8 8 8 8 8 8	3 6 8 6 8 6 8	8 8 8 8 8	8 8 8 8 8 8 8 8	8 6 8 6 8 6 8 6
	2521 CCTAGTACCCAGATGGATGGATGGTCTGTTTCTCAGGCCAACGGGACCTAGAATGTGC 2581 TGACTTATTTTTTTTTTGTGATTCTCACTTCTGTTTTTTTT	DD   1°CCACTGTGCCACTGAAGTTTTTGTACAGAGAAGTATTTGGCCATGATGTCCCTCTATTC 2760	Db 2881 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	SEQ ID NO 22  LENGTH: 3073  TYPE: DNA ORGANISM: Mus musculus S-10-322-281-22  Query Match Best Local Similarity 100.0%; Pred. No Matches 2864; Conservative 0; Mismat  y 32 CGTGCTCGGGTGCGGTTGTGACCTCTGAG  L

3 8 3 8 3 8 5 8 5 8 5 8 5 8 5 8 5

	1249 ATTCTCTTAAGAAGTCCCGAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCCGG	1309 CTGAGGATACCTCTTCTCGCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA 1368	1369 AGAAAAAGTCCTCTACCTCGTCAGGGGAGGTACAGGACCCCTCAGGAACTCAGACCGG 1428	y 1429 TGCCTGATACTCCAGGGCAGCCTGTCCCTGCTGTTGTCCTGCTCCCAAGGAAAGGCATCC 1488	y 1489 TTAAGAAGTCTCGACGTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTG 1548	y 1549 GGGAACTCTTAGACGCCAGTGATGTTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTC 1608	1609 CACAGGCTTCAGGGCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT 1668	1669   CCCGCACAGCCTTAGAAGGCACTACCCCTTGGCTCCCTGGACCAACTGGCCT   1728	1729 CCTCCCATCCTGCAGCCCGGCCCCCCCTCAGGGGCTGTGAGTGA	y 1789 TGFCCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAAGGTCTTCCCGAAACCCCACTGA 1848	y 1849 GGGCTGTGTGTGGACAACCTGAGGGGCTTGAGCAGCCTCCCTC	y 1909 agcgatggtgggaaatccttgggggatagctgcttttctctgacagactgccaagag 1968 	y 1969 TGACTGCAGCCTACAGACCCTAGGAATCTGCTCAAAGCTGAGGAAGGGAGA 2028 	y 2029 IGGIGCCCIAGT-ATGGGGTAGGCTCTGAGAGGGTTTGCAGAGGAACCCTGGGTCGGATT 2087	y 2088 CCTCCAGTGAATAGAGTACATCAAGGGCTCTACGTCTGCAGCCTGACTGAACCTGA 2143	y 2144 AAGATGAGAGAAATCGCATTGATGTGGAAAGGAATGGGAACCCTTGCTGCCGAGTGTTA 2203	
GTGACCTCTGAGCCGGGGCTCAGCGCGGCTGCTACTGCTGCCCGACCCACTCCACCCTC [	69 GCCGTCCCGCACCATGGAGTGGTGGTGGTTACACCGGGGGAACCTGGCTCCCTCGG 128  169 CCTCGCCCTGGCCTCGGAGAGCGCCCGGCGCGCACGGACGG	ASCICICATORAGA AGAGA GOGTA AGAGA COSTA CARA CARA CARA CARA CARA CARA CARA CA	GCTACGAGTTCCTGGAGACGCTGCGCAAGGCCACTTACGGGAAGGTGAAGAAGGCACGAG 34	AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGAAAGACAAAATCAAAGATGAGC 	AGGATCTGCTGCACATACGGAGGGGGGAGATTGAGATCATGTCTTCACTCAACCCCCACA		CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGGCCACGGCTGAGGGGGACG	CCAGGATTTCTTCCGAGAGACGTCTGCCCTGCACTACTGCCACAGAACGGATCG	TTCACCGAGATCTCAAGCTGGAAAACATCCTTCTAGATGCCAATGGAAACATCAAGATTG	CTGACTTTGGCCTCTCCGAACCTGTACCACAAAGGCCAAGTTCCTCCAGACGTTCTGTGGGAACTTTTGGCGTTCTTGTGGGAACTTTTTGGCCTCTCCCAACCTGTACAAAGGCAAGTTCTCTGGGAACTTCTGTGGGAACTTGTTCAAAAGGCAAGTTCTGTGGGAACTTCTGTGGAACTAAAGGCAAGTTCTGTGGGAACTTCTGTGGAAGTAAAGTTCCTCCAGAGCTTCTGTGGAAGAAGTAAAGTTCCTCCAAGAGCTAACAAAGTTCTAAAAGTAAAGTAAAGTAAAGAAGAAGAAGAAGAAGAAGA	GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG 82	9 ACAGCTGGTTCTCTGGGCGTTCCTGTACATCCTGGTGCATGGCACCATGCCCTTTGACG	GCCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCCGCCA 94	AGCCGTCCGATGCCTGTGGCCTGATCGGTGCTGTTAATGGTGAACCCCTGGGG 10 AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGCTGTTAATGGTGAACCCCACCCGTCGGG 10 AACCGTCTGATGCTTGTGGCCTGATATGTTTAATGGTGAACCCCACCCGTCGGG 10 AACCGTCTTAATGTTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTTAATGTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAATGTTAAT	CCACACTGAGGATGTAGCCAGTATTGGTGGGTCAACTGGGGTTACACCCACC	0 0 0	y iddicidanidalianalichining den mengarakan da marangaran

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                                                                                                                   0; Gaps
                                                              DB 17; Length 2027;
                                                                                                                3; Indels
                                                           Score 2022.2;
Pred. No. 0;
0; Mismatches
                                                        Query Match
Best Local Similarity 99.9%;
Matches 2024; Conservative
        US-10-343-514-87
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Publication No. US20040132025A1

GENERAL INFORMATION:
APPLICANT: DRUCKER, Daniel J.
APPLICANT: DRUCKER, Daniel J.
APPLICANT: LEFEBARE, Diana L.
TITLE OF INVENTION: AMPK-RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERENCE: DPA-DRUCZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514
CURRENT FILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 60/222,650

PRIOR FILING DATE: 2001-08-03

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

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; Publication No. US20040126762A1; GENERAL INFORMATION:
; APPLICANT: David.W. Morris
; APPLICANT: David.W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer; FILE REFERENCE: 529452010100
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 37278
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Pred. No. 0;
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LOCATION: (1)...(37278)
OTHER INFORMATION: n = A,T,C
US-10-322-281-21
                                                                                                                                                                                                                                                                                                    Query Match 66.8%;
Best Local Similarity 99.9%;
Matches 1940; Conservative
                                                                                                                                                                              TYPE: DNA ORGANISM: Mus musculus FEATURE:
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CTTCAGGGCTCCTCCTCCTCCACGCAAGGCATTCTCAAACTCAATGGCAAGTTCTCCGCA

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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Bandaru, Rajasekhar
ITILE OF INVENTION: NOVEL 2190, 56634, 55053, 2504, 15977,
ITILE OF INVENTION: NOVEL 2190, 56634, 55053, 2504, 15977,
ITILE OF INVENTION: NOVEL 21907, 11903, 3100, 21529, 26176, 26343, 56638
ITILE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: MPIO3-0230M1M
CURRENT APPLICATION NUMBER: US/10/423,543
CURRENT FILING DATE: 2003-40-25
FRIOR APPLICATION NUMBER: US 09/711,216
FRIOR APPLICATION NUMBER: US 09/711,216
FRIOR APPLICATION NUMBER: US 09/711,216
FRIOR APPLICATION NUMBER: US 06/205,447
FRIOR PILING DATE: 2000-11-09
FRIOR PELING DATE: 2000-11-13
FRIOR APPLICATION NUMBER: US 60/248,325
FRIOR APPLICATION NUMBER: US 60/248,325
FRIOR APPLICATION NUMBER: US 60/248,93
FRIOR PILING DATE: 2000-11-14
FRIOR PILING DATE: 2000-11-15
FRIOR PELING DATE: 2000-11-15
FRIOR APPLICATION NUMBER: US 60/248,93
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FRIOR APPLICATION NUMBER: US 60/248,93
FRIOR PILING DATE: 2001-11-15
FRIOR APPLICATION NUMBER: US 60/248,035
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FRIOR APPLICATION NUMBER: US 60/248,035
FRIOR PILING DATE: 2000-11-15
FRIOR PILING DATE: 2000-01-15
FRIOR FILING DATE: 2000-01-15
FRIOR FILING DATE: 2000-02-28
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Best Local Similarity 81.8*; Fred. No. 0;
Matches 1654; Conservative 0; Mismarcheo
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; LOCATION: (1)...(3333)
; OTHER INFORMATION: n = A,T,C or G
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                                                     CCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGGGGTCTGGTGGCCATCAAGTCCA
                                                                                                                      435 TCATGTCATCACCACCCTCACATTGCCATCCATGAAGTGTTTGAGAACAGCA
                                                                                                                                                                                                                                                                          495 GCAAGATCGTGATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCG
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                    GTGGGGATCCCAAGGAGCAGAAGCCTCCGCAAGCCTTCAGGGCTCCTCCTCCTCCTCGCAAG
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Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: DNA
ORGANISM: Homo sapiens
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Pred. No. 0;
0; Mismatches 338; Indels
                                                                                                           Query Match
Best Local Similarity 81.6%;
Matches 1651; Conservative
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                             Homo
                          ORGANISM: Homo
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Patin Docket Preview

APPLICANT: BODARY, SARAH C.

APPLICANT: CLARK, HILLARY

APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: SCHOENFELD, JILL R.

APPLICANT: SCHOENFELD, JILL R.

APPLICANT: WOOD, WILLIAM I.

APPLICANT: WOOD, WILLIAM I.

APPLICANT: WOOD, WILLIAM I.

TITLE OF INVENTION: Related Diseases

TITLE OF INVENTION: Related Diseases

TITLE OF INVENTION: 2003-02-21

CURRENT APPLICATION NUMBER: US/10/370,715B

CURRENT FILING DATE: 2003-02-21

SEQ ID NOS: 742

LENGTH: 3443
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Pred. No. 0;
0; Mismatches 338; Indele
                                                                                                        APPLICANT: WHYTE, DAVID
APPLICANT: WANNING, GERARD
APPLICANT: CARNEPEEL, SEAN
TITLE OF INVENTION: NOVEL KINASES
FILE REFERENCE: 034536-0321
CURRENT APPLICATION NUMBER: US/10/618,941
CURRENT FILING DATE: 2003-07-15
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 11
                                  ; Sequence 11, Application US/10618941; Publication No. US20040197792A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 81.6%;
Matches 1651; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-11
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1215 GCACCACCCTGGGCCTGGAGCGCCAGCATTCGCTCAAGAAGTCCCGCAAGGAGAATGACA
                                                                                CTAGIGGIGACTITGGCCGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCCC
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Shirley A.  Yalda Jennifer L.  Megan Vicki S.  ILU, Kavitha alg H.  HUMAN KINASES 7125 PCT 7202-12-10  MHBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 7000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-07; 7202-12-10  MHBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 7000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-07; 7000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-07; 7000-06-16-06-06-06-06-06-06-06-06-06-06-06-06-06	OTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CB1   US-10-311-034-38   US-10-311-034   US-10-311-034   US-10-311-034   US-10-311-034   US-10-311-034   US-10-311-034   US-10-311-034   US-10-311-034   US-10-311-0	32 CCTACGGGAAGGTGAAGAGCACGAGGGCCTCGGGGCCTCTGGTGCCACAAGTCCA 36 CCTACGGGAAGGTGAAGAGCACGAGGAGGCCTCGGGGCCTCTGGTGCCATCAAGTCCA 266 CCTACGGGAAGGTGAAGAGCGCGGAGAGCTCGGGGGCCTCTGGTGCCATCAAGTCCA 36 CCTACGGGAAGGTGAAGATGAGCAGGAGCTGCTGCTGGTGCCATCAGGAGTTCAAG 37 TCAGGAAAGAAATCAAAGATGAGCAGATCTGCTGCTGCACATACGGAGGAGATTGAGA 37 TCAGGAAAGACAAAATCAAGATGAGAATCTGATGCACATACGGAGGAGATTGAGA 442 TCATGTCTTCACACACACCCCCCACATCATTGCCACACATACGGAGGAGATTGAGA 445 TCATGTCTTCACACACCCCCACATCATTGCCATCCATGAGAATTGAGAAATAGCA 502 GCAAGATTGTCATGGAGTATGCCAGCCGAGGCGATCTTATGACAACACAGC 503 GCAAGATTGTCATGGAGTATGCCAGCCGGGGCGATTTCTTCCGACAGATCGTGCCC 61

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Db   1697   CAGGGGCTGTGAGCGAGGACCTCTTGACCTTGACCAGCTGGACTTGC   1756	RESULT 14 US-09-963-159-3 US-09-963-159-3 Squence 3, Application US/09963159 Factor No. US20020077312A1 GENERAL INFORMATION: APPLICANT: Curtial, Rory A.J. APPLICANT: Curtial, Ratherine M. TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR FILE REFERENCE: 10147-50U1 CURRENT APPLICATION NUMBER: US/09/963,159 CURRENT FILING DATE: 2001-09-25 PRIOR FILING DATE: 2000-09-25 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver: 2.1 SEQ ID NO 3 LENGTH: 1884 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA TYPE: DNA	Query Match Query Match Best Local 169 229 7 229 7 229 7 289 7 409 0 275 7 469 0 335 7 529							

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84.2%; Pred. No. 0;
ive 0; Mismatches
NUMBER OF SEQ ID NOS: 119
; SOFTWARE PastSEQ for Windows Version 4.0
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; LENGTH: 1884
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Best Local Similarity 84.2
Matches 1565; Conservative
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CGCAAGCTTCAGGGCTCCTCCTCCATCGCAAGGCATCCTCAAACTCAATGGCAAGTTCT 1525
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Libermann, Rosana K.
APPLICANT: Libermann, Rosana K.
APPLICANT: Libermann, Rosana K.
APPLICANT: Mayers, Rachel E.
APPLICANT: Rudolph-Owen, Laura A.
APPLICANT: Cland, Parker and Cland, Parker and Cland, Papell Cant.
APPLICANT: Cland, Ratherine M.
APPLICANT: Cland, Milliamson, Mark J.
APPLICANT: Glalvin, Katherine M.
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TITLE OF INVENTION: 14760, 23551, 11993, 3700, 21529, 26176, 26341
APPLICANT: Milliamson, Mark J.
TITLE OF INVENTION: More APPLICANTON WINDER: US 10/219, 636
PRIOR APPLICANTON WUMBER: US 60/226, 447
PRIOR APPLICANTON WUMBER: US 60/248, 325
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICANTON WUMBER: US 60/248, 325
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICANTON WUMBER: US 60/186, 061
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PRIOR PLING DATE: 2000-03-29
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AX381029 AX430369

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Distribution 1 (Dasses 1 to 2902)

Bird, T.A., Virca, G.D., Martin, U. and Anderson, D.M.

Bird, T.A., Virca, G.D., Martin, U. and Anderson, D.M.

Methods for identifying compounds that alter kinase activity

Patent: US 6514719-A 4 04-FEB-2003;

Location/Qualifiers

1. 2902

/ organism="unknown"
/mol_type="genomic DNA"
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Seguence 4 from patent 1
AR279568
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AUTHORS
TITLE
JOURNAL
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                                                                           January 24, 2005, 14:50:33; Search time 12179.3 Seconds (without alignments) 11267.845 Million cell updates/sec
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                                                                                                                      GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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linear

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2902 bp 4 from patent US 6514719.

ALIGNMENTS

Query Match Len 29 100.0 71.2 69.7 61.0 54.9 2820.4 2063.8 20063.8 20026.9 11701.4 11873.2 11375.8 11375.8 11374.2 11374.2 11374.2 11374.2 11374.2 11370.6 11360.2 Score 2902 Result

Query Match 100.0%; Score 2902; DB 6; Length 2902; Best Local Similarity 100.0%; Pred. No. 0;	Matches 2902; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Oy 1 CACTAGTGGATCCAAAGAATTCGGCACGAGGCGTGCTCGGGTGCGGCTGTGACCTCTGAG 60		Db 1 CACTAGTGGATCCAAAGAATTCGGCACGAGGCGTGCTCGGGTGCGGCTGTGACCTCTGAG 60		Qy 61 CCCGCGGCTCAGCGCGCGCTGCTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCA 120		Db 61 CCCGCGGCTCAGCGCGCGCTGCTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCA 120		Qy 121 CCATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGCCTCCCTC		Db 121 CCATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGGCTCCCTCGGCCTCCGCCCTGG 180		Qy 181 CCTCGGAGAGCGCCCGGCCGCTGGCGGACGGCCTCATCAAGTCGCCTAAACCTCTGATGA 240		Db 181 CCTCGGAGAGCGCCCGGCCGCTGGGGGCTCATCAAGTCGCCTAAACCTCTGATGA 240		OY 241 AGAAGCAGGGGGTGAAGCGGCACCATCACAAACACAACCTGCGGCACCGCTACGAGTTCC 300	
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QYFCGSPLYASPEIVNGKPYVGPEVDSWSLGYLLYILVHGTWPFDGQDHKTLVKQISN
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PVPAVSLLPRKGILKKSRQRESGYYSSPEFSESGELLDASDVFVSGDPVEQKSPQASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be found
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ESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEGLKRWWQBSLGDSCPSLTDCQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIAN at: http://image.llnl.gov Series: Plate: Row: Column: 0
This clone was Row: Column: 0
This clone was passed for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27229181.

Location/Qualifiers

1. 2938

/organism="Mus musculus"
/mol type="mRNA"
/gtrain="C57BL/6"
                                                                                                                                                                                                                                                                                                Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaloc.M.F., Akabogu.I., Bair.T., Bair,J., Crouch,K., Davis,A.,
Fishlar,K., Keppel,C., Kucaba T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /inote="S_TKC; Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine-specific kinase subfamily. The enzymatic activity of these protein kinases is controlled by phosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xrefe="taxon:10090"
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Gene, Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.2%; Score 2820.4; DB 10; Length 2938;
                                                                                            http://mgc.nci.nih.gov
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                                                                                         NIH-MGC Project URL: ht
Contact: MGC help desk
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E.
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COMMENT
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Strausherg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G.,
Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D.,
Klausner, R. D., Collins, F. S., Wagner, L., Schaefer, C. F., Bhat, N. K.,
Hopkins, R. F., Jordan, H., Moore, T., Wans, S. I., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L.,
Staplecon, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L.,
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Carnindi, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J.,
Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J.,
Morkernan, K. J., Malek, J. A., Gunarane, P. H., Richards, S. W.,
Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
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Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E.,
Schnerch, A., Scheln, J. E., Jones, S. J. and Marra, M. M.
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Mus musculus RIKEN cDNA 1200013B22 gene, mRNA (cDNA clone MGC:61244
MAGE:6816569), complete cds.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 2938)
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Direct Submission
Submitted (13-FEB-2003) National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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VERSION
KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
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BC046833
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Best Local Similarity 99.1%; Pred. No. 0; Matches 2855; Conservative 0; Mismatches 1; Indels 24; Gaps 1;	43 GCGGCTGTGACCTCTGAGCGCGCGCGCGCTGCTGCTGCTGCCGACCCACTC 102 	103 CACCTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTACTCCAGCGCCCGAGCCAGGCTC 162		TGAAGCGGCACCATCACAAACACAACCTGC	SCAAGGGCACTACGGGAAGGTGAAGAGGTGAAGGGCACTACGGGAAGGTCAAGGGCACTACGGGAAGGTGAAGAAGGTGAAAAAGGTGAAAAAGGTGAAAAAGGTGAAAAAGGTGAAAAAA					GTGAGCGCCACGGCTGAGTGAGCGGACGCCAGGCATTTCTTCCGACAGATCGTGTCTC		TTCTAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACA			TCTGGTGCATGGCACCATGCCTTTGACGGGCAGATCATAAACACTGGTGAGCAAA		GGCTGTTAATGGTGAACCCCACCGTCGGGCAACTGGAGGATGTAGCCAGTCATTGGT 	GGGTCAACTGGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGGTGGGC
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TACGTCGCTCCTCGCGCC 1158 AGCACGTGCCGGGAGGTG 1218 CCCTGCGTGAGGGTGGGC 1080 CTTCTCGCCCTGGCAAGA 1338 CTACCTCGTCAGGGGAGG 1398 ACGCCAGTGATGTTTG 1578 CAGCCCAGCCCACCCC 1758 CAGGGCAGCCTGTCCCTG 1458 CAGGGCAGCCTGTCCCTG 1440 TAGAAGGCACTACCCCTA 1698 |||||||||||||||||| TAGAAGGCACTACCCCTA 1680 AGGAATCCTTGGGGGATA 1938 ATGGGGTAGGCTCTGAGA 2058 SAGTACATCAAGGGCTCT 2118 ATTGATGTGGAAAGGAAT 2178 ACAGACAAGCCCTAGGAA 1998 ACAGACAAGCCCTAGGAA 1980

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Contact: MGC help desk
Email: cgapba-r@mail.nih.gov
Issue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergran, B.J., Lu, X., Glbbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, B. Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Gennerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iocation/Qualifiers

1. 2917

/organism="musuculus"
/mol type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="MGC:30598 IMAGE:3663595"
/tissue_type="Mammary tumor metastatized to lung.
mMTV-LTR/mtl model. Expression driven by an MMTV-LTR
enhancer."
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/lab_host="DH10B"
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Strausberg, R.
Direct Submission
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

El (bases 1 to 2917)

Straubberg, R.L., Feingold, E.A., Grouse, L.H., Derge, JG.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, JJ., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., F.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Parnge, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Mus musculus RIKEN cDNA 1200013B22 gene, mRNA (cDNA clone MGC:30598
IMAGE:3663595), complete cds.
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                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                Length 2929,
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Pred. No. 0;
0; Mismatches 277; Indels
                                                                                               Drucker, D.J., Rosen, C.F. and Lefebvre, D.L.
Ampk-related serine (threonine kinase, designated
Patent: WO 0212456-A 1 14-FEB-2002;
1149336 ONTARIO INC. (CA)
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/organism="Rattus sp."
/mol_type="unassigned D
/db_xref="taxon:10118"
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Rodentia;
              GI:19575800
                             Rattus sp.
Rattus sp.
Bukaryota; Metazoa; C
Mammalia; Butheria; R
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Best Local Similarity 86.4%;
Matches 2488; Conservative
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                                                             CAGCCTACAGACACAGGGAATCTGCTCGAAGCTCAGCTGAGGAAGGGAAGATGGTGC
                                                                                               CCTAGTATGGGGTAGGCTCTGAGAGGGTTTGCAGAGGAACCCTGGGTTCGGATTCCTCCAG
                                                                                                            CCTAGTATGGGGTAGGCTCTGAGAGGGTTTGCAGAGG-ACCCTGGGTCGGATTCCTCCAG
                                                                                                                                                             CCATCTCTGCTGCTGCATCTCAAAGACCTGGGAAGACTCGGACCGCTGTTTGACTTCA
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                                               CAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAAGGGAGATGGTGC
                                                                                                                                                TGAATAGAGTACATCAAGGGCTCTACGTCTGCAGCCTGAACCTGAAAGATGAGAGA
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CTGATTTTTGGCCTCTCCAACCTGTATCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGGA GCCCTCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG

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18-MAR-2002

PAT

linear

DNA

AX380960 2929 bp Sequence 1 from Patent WO0212456.

RESULT 4
AX380960
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DEFINITION

AN381046  MA381046  A381046  MA38104
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		1069   GGGAACAGGAAGCCCTGCGTGAGGCACCCTAGTGGTGACTTTGCCCGGCCCTCCA   128   1128
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	RESULT 6 AX380986 LOCUS LOCUS DEFINITION Sequence 27 from Patent W00212456. AX380986 AX38098 AX38098 AX38098 AX38098 AX38098 AX38098 AX38098 AX3809	Ouery Match Best Local Similarity 93.1%; Pred. No. 0; Matches 1888; Conservative 0; Mismatches 136; Indels 5; Gaps 3;  Qy 49 GTGACCTCTGAGCCGGGGCGCTGCTGCTGCCGCGCCCCCCCC

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l (Dades I to 291162).

Muzny, D. Marte., Metzer, M. Lee., Abramzon, S., Adams, C., Alder, J., Alebrooks, S., Amin, A., Anguiano, D., Anyalebechi, W., Aoyagi, A., Ayogaji, M., Baca, E., Baden, H., Balderin, C., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bharch, C., Burch, P., Burrell, K., Calderon, E., Cardens, V., Carter, K., Cavazos, I., Casar, H., Center, A., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dengado, O., Denson, S., Deramo, C., Toyle, M., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabiei, A., Ganta, R., Garer, M., Garer, M., Gabiei, A., Gante, R., Gardy, M., Garer, M., Gabiei, A., Gante, R., Handland, M., Hanil, C., Hamilton, C., Hamilton, K., Harlak, P., Hawes, A., Henderson, N., Hernandez, J., Howells, S., Huldun, S.L., Hodgson, A., Hogues, M., Hones, S., Hladun, S.L., Hodgson, A., Hogues, M., Jang, H., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Liu, J., Liu, J., Liu, J., Liu, Y., Longacre, S., Lopez, J., Liu, J., Liu, Y., Liu, Y., Longacre, S., Lopez, J.,
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291762 bp DNA linear HTG 15-NOV-2002
Rattus norvegicus clone CH230-274J3, *** SEQUENCING IN PROGRESS
**** 13 unordered pieces.
                                                                                         CCTCCCATCCTGCAGCCCGGCCCCCTCAGGGGCTGTGAGGACAGCATCC 1788
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus (Norway rat)
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Libert Submission of the and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA

On Nov 15, 2002 this sequence version replaced gi:23269681.

The sequence in this assembly is a combination of BAC based reads and whole genome shocgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/ratl). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and the feature table.
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
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Mandiney, S., McLeod, M.P., McNeill, T.Z., Menen, E.,
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Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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Valas, R., Vera, V., Villasan, D., Walter, R., Walte, F.,
Williams, G., Willson, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yon, L.,
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Walter, Submission
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Direct, Submission
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Leger, J., Shon, Y., Salab, R., S.,
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* Consists of 13 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Center code: BCM
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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18 271861; gap of unknown lenger
18 276281; contig of 1405 bp
18 276287; contig of 1519 bp
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24 280724; contig of 1314 bp
25 280624; gap of unknown lenger
25 284658; contig of 1314 bp
25 284758; gap of unknown lenger
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612 TGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTTCAAGCTGGAAAACATCCTTC  [	10.000   1
Db 276114 AGTCTCGACAGCGTGAATCTGGTTACTCCTCTCCAGGGCGCAGCGGGAAC 276173  Oy 1555 TCTTAGACGCCAGTGATGTGTTTGTGAGCGCACCCGGGAACTCCCACGG 1614  Db 276174 TCTTAGACGCCAGTGATGTGTTTGTGAGCGCACCCGTGGAGCAGACTCCCACAGG 276233  Oy 1615 CTTCAGGCGCCAGTGATGTGTTTGTGAGCGCACCCCGTGGAGCAGACTCTCACACGG 276233  Oy 1615 CTTCAGGGCTCCTCCCCCCCAAGGGCATTCTCAAACTCAATGGCAAGTTCT 1668  Db 276234 CTTCAGGGCTCCTCCCCCCCAAGGGCATTCTCAAACTCAATGGCAAGTTCT 276287  RESULT 8  AX407116 AX407116 3353 bp DNA linear PAT 14-JUN-2002  DEFINITION Sequence 1 from Patent W00224921.  DEFINITION Sequence 1 from Patent W00224921.  PRESCORNON AX407116 GT:21439882  CCCSSION AX407116 GT:21439882  CCCSSION AX407116 GT:21439882  CCCSSION AX407116 GT:21439882  CCCSSION AX407116  AMATOTAGAGCTCCTCCTCCACGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT 276287  CCCSSION AX407116  AAUTHORS Homo sapiens (human)  AUTHORS Homo sapiens (human protein kinase and uses therefor human protein kinase and uses therefor JOURNAL Patent: W0 0224921-A 1 28-WAR-2002;  Millennium Pharmaceuticals, Inc. (US)  CCCTCOATOM/Qualifiers  COATOM/DEATS AND SAPIENS  CAALOM/DEATS AND SAPIENS  CAALOM/DEATS AND SAPIENS  CAALOM/DEATS AND SA	Query Match

141 136 201 184 261 244 321 304 381 364 441

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TGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTCAAGCTGGAAAACATCCTTC 681
                                       CTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTAC
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                                                                                                                 142 TCCAGCGCCCGAGCCAGGCTCCCTCGGCCTCGGCCTCGGAGAGAGCGCCCGGCCGC
                                                                                                                                                                                                                                                                       ACCATCACAAACACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAAGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                          425 TCATGTCATCACTCAACCACCCTCACATTGCCATCCATGAAGTGTTTGAGAACAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 AGGGGAGCAGCTCAGTGAGCGGGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCG
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| /db xref="G1:45502722"
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DDTAHRPGKSNLKLPKGILKKKVSASAEGVQEDPPELSPIPASPGQAAPLLPKKGILK
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PLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPLGDSCFSLTDCQEVTATYRQALRVC
SKLT"
                                                                                                                                                                                                                                                                                                                             SAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHOGRFLQTFCGSPLYASP
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CGLIRWLLMVNPTRRATLEDVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAD
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                 TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                        CCTTCGCTCCCTGGATGAACTCGCCCCACTTGCCCTGGCCCGGGCCAGCCGA
                                                                         CAGGGGCTGTGAGGACAGCATCCTGTCCTCCGAGTCCTTTGACCAATTGGACTTGC
                                                                                                                                                   TTGAGCAGCCTCCCTCAGAAG------GTCTGAAGCGATGGTGGCAGGAATCCT
                                                                                                                                                                                                                                                                                                                                                                                  CCCTAGGAATCTGCTCAAGCTCAGCTGAGGAAGGGAGATGGTGCCCTAGTATGGGGTAG
CCTTTGGCTCCCTGGACCAACTGGCCTCCCATCCTGCAGCCCGGCCCAGCCGCCCT
                                                                                                             caddedecrercadedadadadadadarecrercadarecrirreacedecreaciree
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EP 1396543-A 2518 10-MAR-2004;
Association for Biotechnology (JP)
Location/Qualifiers
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Sequence 2918 from Patent EP1396543.
CQ782778
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Pred. No. 0;
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1187. .2004
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Best Local Similarity
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

CQ782778 LOCUS

RESULT

ORGANISM

REFERENCE AUTHORS

source

CDS

FEATURES

TITLE JOURNAL

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561 544 621 604 664 741 724 801 861 844 921

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1144

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ORIGIN

1041 1024 1101 1084 1161

981 964

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07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO ISHII,
ISHII,
YURI KAWAI,AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI
   Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 3395)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC C12P21/02,C12Q1/68/C12P21/08,G06F17/30,C12N15/00,C12NS/00
Primer for synthesizing full-length cDNA and use thereof FH K Location/Qualifiers
T CDS Location/Qualifiers
Location/Qualifiers
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                                                                                                                                                                                                                                                            Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002017375-A 2740 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
JP 2002017375-A/2740
22-JAN-2002
sapiens (human)
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Query Match 47.4%; Score 1375.8; DB 6; Length Best Local Similarity 81.7%; Pred. No. 0; Matches 1652; Conservative 0; Mismatches 337; Indels
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PAT\_18-SEP-2002

BD127309 3395 bp DNA linear PAT 1 Primer for synthesizing full-length cDNA and use thereof. BD127309.1 GI:2322254 JP 2002017375-A/2740.

RESULT 10 BD127309 LOCUS DEFINITION ACCESSION VERSION KEYWORDS

1989 1975

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Is 2 (Dases I to 3395)

Is 2 (Dases I to 3395)

Is 1 sogai, T. and Oteuki, T.

Direct Submission

L. Submitted (125-MAR-2002) Takao Isogai, Helix Research Institute,

Submitted (25-MAR-2002) Takao Isogai, Chiba 292-0812, Japan

Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:181-438-52-3975, Fax:811-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; cDNA full insert sequencing:

Research Association for Biotechnology; cDNA full insert sequencing:

Institute of Medical Science, University of Tokyo, Laboratory of

Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass

sequencing and clone selection: Helix Research Institute (supported

by Japan Key Technology Center etc.).
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Catarrhini, Hominidae, Homo.
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/cell_type="teratocarcinoma"
/clone_lib="NT2"
/clone_ilb="NT2"
/note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
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/clone="NT2RP2003179"
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Mammalia; Eutheria; Primates;
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: o Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13569921. Location/Qualifiers
    Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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SAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASP
EIVNGKPYTGPEVDSWSLGVLLXILVHGTMPPDGHDHKILVKQISNGAYREPPKPSDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 ACCACCACAAGCACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCGGACGGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein DKF2p434J037"
/protein id="AAH17306.1"
/db_xref="G1.168798206"
/db_xref="LocusID:81788"
/db_xref="NM:608131"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/b xref="taxon:960"
/clone="MGC:29812_IMAGE:5088037"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="gNARK"
/ncte="gynonym: DKEZP434J037"
/db_xref="LocusID:81788"
/db_xref="MIM:608131"
100. .1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Lymph, lymphoma
/clone_lib="NIH MGC_99"
/lab_host="BH10B"
/not=="Vector: pOTB7"
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/codon_start=1
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1 (bases 1 to 3402)

2 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.R., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Katyainski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Schein, J.E., Jones, S.J. and Marra, M.A. M. M. M. Ammalyais of more than 15,000 full-length hyman and mouse only
                                                                                                                                      TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG 1989
                                                                                                                                                                                                                                                                                                                     2049
                                                                                                                                                                                                                                                                                                                                                                                                  CACTGAGGGTCTGCTCAAAGCTCACCTGAGTGGAGTAGGCATTGCCCCAG-CCCGGTCAG 2034
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3402 bp mRNA linear PRI 29-JUN-2004

Homo sapiens likely ortholog of rat SNF1/AMP-activated protein

kinase, mRNA (cDNA clone MGC:29812 IMAGE:5088037), complete cds.
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Submitted (05-NOV-2001) National Institutes of Health, Mammallan
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov/
Context: nisc.mgc@nhgri.nih.gov/
Akhter,N., Ayele,K., Becketrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Boulfard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
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Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:16878205.
Contact: MGC help desk
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12477932
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TITLE
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196GGGGATAGCTGCTTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG 1989
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Catarrhini; Hominidae; Homo.
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                                                                                       ACTCCTCTCCCGAGCCCAGTGAATCTGGGAGCTCTTGGACGCAGGCGACGTGTTTGTGA
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Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Bugas, M., Ells, R., Brors, B. and Mergenthaler, S. Novel genetic arrivers for leukemias Patent: WO 03039443-A 2508 15-MAY-2003; Deutsches Krebsforschungszentrum (DE); Ludwig-Maximilian-Universitaet Muenchen (DE); PD Dr. (DE); Schoch, Claudia (DE); Kern, Location/Qualifiers
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                                                                                                                                                         0; Mismatches 338;
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                                                                                                               Score 1374.2;
Pred. No. 0;
      /gene="DKFZp434J037"
3399
/gene="DKFZp434J037"
                                                                                                               Query Match
Best Local Similarity 81.6%;
Matches 1651; Conservative
                            polyA_site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This close (DKFZp434J037) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available thrup://mips.gsf.de/proj/cDNA/.
CCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGAATGGTGCCCTAGTATGGGGTAG 2049
                      HSM801859 3443 bp mRNA linear PRI 20-MAR-2002
Homo sapiens mRNA; cDNA DKFZp434J037 (from clone DKFZp434J037);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              German
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HANDLARPEELETLGKGTYGKVKKARESGGRLVAIKSIKOKKKDEDDLMHIRREIE
IMSSLMHPHITAIHPFENSSKIVIVWEYASRGDLVDYISERQOKEREREREIE
SAVHYCHQNRVVHRDLKLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASP
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CGLIRWLLMVNPTRRATLEDVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMAD
WLRRSSRPLLENGAKVCSFFKQHAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTA
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KPRQRSGYTYSSPEPSESGELLDAGAVFVSGDPKGKPQPGAGGGLLLHKKGILKLKGKF
SQTALELAAPTTFGSLDELAPPRPLAKASTSGAVSEDSILSSBSFDQLDLPERLPEP
PLRGCVSVDNLTGLEEPPSEGPGSCLRRWRQDPLGDSCFSLIDCQEVTAYRQALRVC
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 343)

Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S. Direct Submission
Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152
Martingried, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone from S. Wiemann, Molecular Genome Analysis, German Cance
Research Center (DKFZ); Email s wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the
                                                                                                            2050 GCTCTGAGAGGTTTGCAGAGGAACCCTGGGTCGGATTCCTCC
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/clone_lib="434 (synonym: ht
DHIOB, sites NotI + SalI"
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1. .3443
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/gene="DKFZp434J037"
/note="strong similarity
protein kinases"
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CGGAG           CCGAG GGCCT	GGTG1	90000 	TGACC 	CATTC	CAGAC       agaca	AGGCA  - - -  - - -	CGAGT	GAAGT	CAAGT	ACTGG ACTCG	243 	00000000000000000000000000000000000000	AG	TCTGA 	5 	AGGAA     TGCAC
CCAC       CCAC	CCAA	TGGA	PAGG  -   ACAG	AGGG	PACT PAGCT	GGAA.	CCAG	AGCA 	A166	ACCA    -    ATGA	AGGA 	PAACO	CAGA	7777C	S=S	GCAG
TTACA     CTACG	CTCTG TGGAG TGGGG	76660       76600	701-19 101-19 101-01	TCCGA 	TCAGG		AGAGO      CGAGO	CGTGC	ACTCA ACTCA		GAGTO	TCCCG 	7000 11111			GCAGC
GGGG       GGGG	AGTGA HIIII	STACC    VCCCC	AAAA    -   AGTC	AGCT	ACCC HHHH	130 130 130 130 130 130 130 130 130 130		ACCO HATCO	TCAA	60-10 	10 11 11 11 11 11 11 11 11 11 11 11 11 1	19-17-17 19-17-17 19-17-17	AGCC 	ATAG	GGGT	agage 
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Search completed: January 25, 2005, 01:53:15 Job time: 12193.3 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

(without alignments) 11348.500 Million cell updates/sec January 24, 2005, 05:56:58 ; Search time 1342.36 Seconds

US-09-980-464-4

Perfect score:

Sequence:

Gapop 10.0 , Gapext 1.0

IDENTITY NUC

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

4134886 seqs, 2624710521 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

geneseqn2001as:\*geneseqn2001bs:\* genesegn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2003bs:\* N\_Geneseq\_23Sep04:\* geneseqn1980s:\* geneseqn1990s:\* geneseqn2000s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2003cs:\*

geneseqn2004s:\*

SUMMARIES

## Abk14000 cDNA enco Ad114160 Novel hum Ad130885 Full leng Abx71420 Human cel Abx71420 Human cel Ad75964 Novel hum Ad681952 Leukaemia Ad020171 Human PRO Adj96554 Human cal Adm43851 Novel hum Abx1133 Human pol Abx1133 Human pol Ad26459 Human kin Ad114162 Novel hum Ad144659 Novel hum Ad14659 Novel hum Ad14659 Novel hum Ad14659 Novel hum Ad14659 Novel hum Ad14659 Novel hum Aac90433 Murine Ly Aad31710 Rat SNF1/ Description ADL14160 AAK94280 ADF81952 ADC20171 ADJ96554 ADM43851 ADL30885 AAC90433 AAD31710 ABK14000 DB Query Match Length 463 1375.8 1375.8 1374.2 1374.2 1374.2 1374.2 1374.2 1370.2 1370.6 1360.2 Score 2902 2066. Result Š.

Aad14327 Human pro Ade38420 Human pro Adn95767 Human BEC		Human Human Human C	Human c	Adl28314 5' end of Aad03994 Human pro Abl21269 Drosophil	Aah13802 Human cDN Aaf44655 Novel pro Aa160326 Human 207	Adi29353 Mouse MAR Aba05737 Murine ne Aba05738 Murine ne	
AAD14327 ADE38420 ADN95767		ADQ23883 AAD14328 AAK93296	AAK91887 ADL29723	ADL28314 AAD03994 ABL21269	AAH13802 AAF44655 AAL60326	ABA05737	ABS64386 AAD51409 ADG91747
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2222	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3326	332	3 3 4 9 55	33 38 39	4 4 4 0 1 2	44 45 45

## ALIGNMENTS

RESULT 1 AAC90433

AAC90433 standard; cDNA; 2902 BP.

AAC90433;

19-MAR-2001 (first entry)

Murine Lymph node Stromal cell kinase 1 coding sequence. 

Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder; wound healing; periodontal disease; inflammatory disease; tumour; infection; allergy; ss.

Mus musculus.

WO200073468-A1.

07-DEC-2000.

26-MAY-2000; 2000WO-US014696.

99US-0136781P 28-MAY-1999;

(IMMV ) IMMUNEX CORP.

Bird TA, Virca GD, Martin U, Anderson DM;

WPI; 2001-061546/07. P-PSDB; AAB50056 Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.

Claim 1; Page 86-87; 106pp; English

The present sequence is the coding sequence for Murine Lymph node Stromal cell kinase 1 (MLSK-1). The protein encoded by the present sequence is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal infection

Abz77163 Human pro Abg72599 Human MDD Abg72698 Human MDD

ABZ77163 ABQ72599 ABQ72698

AAF75338

1349.2 1323.2 1230 849.2 849.2

ADL14162 AAF44659

ABZ11333 AAD26459

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	0; Db 1021 60 Oy 1081 60 Db 1081	60  Qy 1141 TACGTCGCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGG 120  Db 1141 TACGTCGTCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGG	180 Qy 1201 180 Db 1201	240 Qy 1261 240 Db 1261	300 1321 CTTCTCGCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAGTCCT 300 Db 1321 CTTCTCGCCTGGCAAGAGCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAGTCCT 300	360 1381 CTACCTCGTCAGGGAGGTACAGGAGGACCCTCAGGAACTCCAGGACCCGTGCCTGATACTC  1381 CTACCTCGTCAGGGAGGTACAGGAGGACCCTCAGGAACTCCAGGAACTCCAGGAACTCAGACCCTCAGACCCCTCAGACCCCTCAGACCCCTCAGACCCCTCAGACCCCTCAGACTCAGACCCTCAGAACTACACTCAGAACTACAGAACTACAGAACTACAACTAGAACTACAGAACTACAGAACTACAGAACTACAGAACTACAACA		64 4		99				1761 006	900 DP 1981 DP 1981
554 A; 794 100.0%;	imitarity 100.0%; Fred. No. 0;  ; Conservative 0; Mismatches 0; Indels 0;  CACTAGTGGATCCAAGAATTCGGCACGAGGCGTGCTCGGGGTGCGCTGTGACCT	1 CACIMENTAL CANAGE AND TRESCREGAGE GREET CONTROLLE AND TREE CONTROLLE AND TREE CANAGE AND TRE	121 CCATGGAGTCGGTGGCTTACTCCAGCGCCCGAGCTGGCTTCCTCGGCCTCGGCTGGCT	181 CCTCGGAGAGCGCCCGGCCGCTGGCGGACGGCTCATCAAGTCGCCTAAACCTCTGATGA 	241 AGAAGCAGGTGAAGCGGCACCATCACAAACACACAGCTGCGGCACCGCTACGAGTTCC	301 TGGAGACGCTGGGCAAGGGCACCTACGGGAAGGTGAAGAAGGCACGAGAGACTCGGGGC 	361 GTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGCAGGATCTGCTGC 1	421 ACATACGGAGGACATTGAGATCATGTCTTCACTCAACCACCCCACATCATTGCCATCC 	AIGAAGTGTTTGAGAATAGCAGCAGGAGATTGTGATTGTCATGGGGGGTATGCGGCGGCGGCGGCGGCGGTTTGTTGTGTTGTGTTGTGTTGT	601 TCCGACAGATCGTGTCTGCCCTGCACTACTGCCACGAGACGGGATCGTTCACCGAGATCG	661 TCAAGCTGGAAAACATCCTTCTAGATGCAATGGAAACATCAAGATTGCTGACTTTGGCC 	721 TCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGTGGAGCCCTCTTACG		1666CG11C1CC1G1ACA1CC1GG1GCA1GCATGCCCTTTTGACGGGCAGG	841 1955CGTTCTCCTGTGTCCTGGTGCATGCCCTTTGACGGGCAGGATCATA 901 AAACACTGGTGAAGCAATCAGTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATG

/\*tag= a /product= "Rat SNARK protein"

Location/Qualifiers

. .1975 /\*tag=

Key

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        GAGTACATCAAGGGCTCTACGTCTGCAGCCTGAACCTGAAAGATGAGAAATCGC
                 GGTGCCTACCTCCTTTGTGCCATGAGTGTCACCCATGACATTTCCCACCCTGTTCTCTGG
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AMPK (AMP-activated protein kinase)-related kinase, designated SNARP polypeptides and polynuclectides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.

Example, Fig 2; 94pp; English

Lefebvre DL;

Rosen CF,

Drucker DJ,

WPI; 2002-241747/29. P-PSDB; AAE19885

03-AUG-2000; 2000US-0222650P 12-MAR-2001; 2001US-0274613P. 28-MAR-2001; 2001CA-02340783.

(ONEO-) 1149336 ONTARIO INC.

02-AUG-2001; 2001WO-CA001109

WO200212456-A2

14-FEB-2002

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The invention relates to an AMPK (AMP-activated protein kinase) related kinase, designated SNARK polypeptides and polynucleotides. SNARK (SNIF/AMP-activated protein Kinase) is involved in stress response to glucose deprivation. The polynucleotides are useful for expressing SNARK protein in isolated form or as a protein conjugate. Activation of SNARK primates liver CPT-1 thus enhances lipid metabolism in liver cells and in other cell types such as heart and skeletal muscles, as well as in other cell types such as heart and skeletal muscles, as well as increases GLUT-4 and glycosen in muscle. Activation of SNARK is predicted in chave insulin-like effects that would enhance the disposal of glucose into muscle and reduce plasma glucose for the treatment of diabetes and some type of disorders of lipoprotein production leading to increased come type of disorders of lipoprotein production leading to increased administered to a subject to treat or prevent a disease associated with decreased expression of SNARK, such as disbetes. SNARK antibodies are used to modulate SNARK activity either in vivo for therapeutic purposes. SNARK antagonists may be administered to increase fuel production, decrease glucose uptake and increase levels of blood glucose in a patient suffering from hypoglycaemia. The present sequence is rat SNARK CDNA suffering from hypoglycaemia. The present sequence is rat SNARK CDNA
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Pred. No. 0;
0; Mismatches 277; Indels 115; Gaps
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Best Local Similarity 86.4%;
Matches 2488; Conservative
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14; 108

168 128

Rat; SNF1/AMPK-Related Kinase; SNARK; enzyme; stress response; diabetes; glucose deprivation; lipid metabolism; therapy; lipoprotein disorder; hyperglycaemic; drug screening; hypoglycaemia; ss.

SNF1/AMPK-Related Kinase (SNARK) cDNA.

(first entry)

18-JUN-2002

AAD31710;

AAD31710 standard; cDNA; 2929

	8 8 8 8 8	1329 AGAAAAAGGCCTCTCCTCATCGGGGGAGGTACAGGAGGCCCTCAGGAACTCAGGACCAG 1388  1429 TGCCTGATACTCCAGGGCTGTCCCTGCTATCCCTGCTCCCAGGAAAGGCATC 1488	999 17 98.
429 TCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATTGTGATTGTCATGGAGTACG 488 529 CCAGCCGAGGCGATCTGTATGATTACATCAGTGAGCGCACGCTGAGTGAG	ପ ଓ ପ	1509 GGGAACTCTTAGACGCAGGTGATGTCTTTGTGAGTGCGCACCCCGTGGAGCAAAGTCTC 1568 1609 CACAGGCTTCAGGGCTCCTCCACCGCAAGGGCATTCTCAAACTCAATGGCAAGTTCT 1668	
589 CCAGGCATTTCTTCCGACAGATCGTCTCCCCTGCACTACTGCCCACCAGAACGGGATCG 648	<i>₹</i> 6 €	9 CCGGCACAGGCTTAGAAGGCACTACCCCTAGGACCTTTGGCTCCCTGGACCAACTGGCCT 172	
649 TICACCGAGAICTCAAGCIGGAAAACAICCTICIAGAIGCCAAIGGAAACAICAAGAITG 708 	S & &	CCTCCCATCCTGCAGCCGGGCCCAGCGGCCTCAGGGGCTGTGAGAGGACAGGATC 178	÷
709 CTGACTTTGGCCTCTCCAACCTGTACCACAAAGGCAAGTTCCTCCAGACGTTCTGGGGA 768	À 8	1789 TGTCTCCGAGTCCTTTGACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGA 1848 	
769 GCCCTCTACGCCTCGCCTGAGATAGTCAACGGGAAGCCCTATGTGGGCCCAGAGGTGG 828 	රු සි	1849 GGGGCTGTGTGTCTGTGGACAACCTGAGGGGGCTTGAGCAGCTCCCCTCAGAAGGTCTGA 1908 	
829 ACAGCTGGTCTCTGGGCGTTCTCCTGTACATCCTGGTGCATGGCACCATGCCTTTGACG 888	ζς q	1909 AGCGATGGTGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGG 1968 	
889 GGCAGGATCATAAAACACTGGTGAAGCAAATCAGTAACGGGGCTTACCGTGAGCGCCC 948	λο q	1969 TGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGGAGA 2028 	
949 AGCCGTCCGATGCCTGTGGCCTGATCCGGTGGACCCCACCCGTCGG 1008	λό da	2029 TGGTGCCCTAGT-ATGGGGTAGGCTCTGAGAGGTTTGCAGGAACCCTGGGTCGGATT 2087 	4.7
1009 CCACACTGGAGGATGTAGCCAGTCATTGGTGGGTCAACTGGGGTTACACCACCGGAGTCG 1068	λo q	2088 CCTCCAGTGAATAGAGTACATCAAGGCTCTACGTCTGCAGCCTGAACCTGA 2143	
1069   GGGAACAGGAAGCCCTGCGTGACGGTGACCCTAGTGGTGACTTTGGCCGGGCCTCCA   1128	& <b>9</b>	2144 AAGATGAGAAATCGCATTGATGTGGAAAGGAATGGGAACCCTTGCTGCCGAGTGTTA 2203 	
1129 TGGGGAACTGGTTACGTCGCTCCTCGGGCCCCTCCTGGAAATGGAGCCAAGGTGTGCA 1188 1089 TGGCGAACTGGTTACGTCGCTCCTCCCCCCTCCTGGAGAATGAACCAAAGTGTTACTACTCTCCTCCTGGAGAAATGAAACCAAAATGAAACTAAAATAAAACAAAAAAAA	& a	2204 TAGTGGGGTGGCCTGAAGGTGCCTACCTTTTGTGCCATGAGTGTCACCCATGACA 2260 	ı q
1189 GCTTCTTCAAGCAGCAGGTGGAAGTGGAAGCACTGTACTGGGCTGGAGGGAAC 1248 [	장 名	2261 TITCCCACCCTGTICTCTGGCTGCACCTCACATAAGITTCTGTTTCCATCA 2312	
1249 ATTCTCTTAAGAAGTCCGAAAGGAGAAATGACATGGCTCAAAATCTGCAAGGTGACCGG 1308 1209 ATTCTCTTAAGAAGTCCCGCAAGGAGAAATGACATGGCTCAAAATCTCACAAAATCAAGAAGTCCCGCAAGGAGAAGTGAATGACATGGCTCAAAATTCAAGAAGAAGAAGTAAATGAAATGACATGAATGA	& A	2313 ACCACCAGGGTTAGAACCCTGACTTCCTGGGAGGTAATGTGTAGTGACTGCATTATTTA 2372 	
1309   CTGAGGATACCTCTTCTCGCCCTGGCAAGAGCGTTAAGCTTCCGAAAGGCATTCTCA   1368	<i>8</i>	2373 GAGAGGAAACAGCCTCTGGTTTCCATCTCTGCTGCTGCATCTCAAAGACCTGGGAAGA 2432 	
1369 AGANAAGTCCTCTACCTCGTCAGGGGAGGTACAGGAGCCCTCAGGAACTCAGACGG 1428	· 경영	2433 CTCGGACCGCTGTTTGACTTCATCTCAAGGGACCAGATGCCCCTGGACCCCATCTTAGA 2492	

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682 TAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACAAAG 741
                                        Claim 28; Fig 1; 115pp;
                    disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; protein kinase 3700; PK; protein phosphorylation; tumourigenesis; cell signalling; mitogenesis; gene transcription; angiogenesis; sarcoma; tissue repair; tissue regeneration; atherosclerossis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157. .2043
/*tag= a
//product= "Protein kinase 3700"
//product= "Protein kinase 3700"
//note= "The coding region (not including the terminator codon) is specifically claimed in claims 7 and 28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of modulators of activity of 3700 protein for making medicament for e.g., modulating protein phosphorylation or cell signaling, or for
                                                                                                                                                                                                                                                                                                                                                        CACTGTCTGGATTGAGTCTCCAGTCCCTTCACACCCAAGGCTGGCCACCCTCCTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTCAGAGACTTGAACCTTGAAGCTGTTCCTAGTACCCAGATGTGGAT-GCTCTGT
                                                    - CTCAGAGACCTGAGCCTTTGATGCTTGATAACCAGACTATGATGGTATGTCTGT
                                                                                                                            rrcrcageccaecaceaearerecreacitarirra--rrrrerearrcrcacrr
                                                                                                                                                                                                         TGAATGCTGTGTTCTGGGGAACTCCACTGTGCCACTGAAGTTTATGTACAGAGAAGTATT
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                                                                                                                                                                                                                                                 -----TITGITIGITIGITIGITITATATAAGIGAATITITGCIGCITICAATAATG
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An area designated 3700, and the polymucleotide sequence encoding it. The invention also describes the use of a modulator of the activity of protein kinase (PK) 3700 for making a medicament or pharmaceutical composition for modulating the ability of a cell to phosphorylate an amino acid residue of a substrate protein. Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylate an amino acid residue of a substrate protein. Modulators of protein kinase 3700 activity are useful for modulating protein phosphorylation, cell signalling, tumourigenesis, mitogenesis, transcription of a gene, progression of atheroselerosis, and signalling across the blood-brain barrier. The polymucleotide and polypepide molecules for protein kinase 3700 may be used as diagnostic targets and therapeutic agents for curing pk-related disorders and cellular pholyficing, alleviating, or curing pk-related disorders and cellular pholyficing, alleviating, or differentiative disorders and cellular pholyficing, and significative and/or couring pk-related disorders and cellular pholyficing, missed 3700 to detect a genetic alteration in a 3700 gene, in chromosome mapping, for transcription, in forensic physical as surrogate markers. The present
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preventing cellular proliferative and/or differentiative
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Pred. No. 8.2e-295;
0; Mismatches 335;
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                                                                                                                                                                                 English
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Best Local Similarity 81.8%;
Matches 1654; Conservative
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Claim 1; SEQ ID NO 43; 139pp; English
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                         2000US-0246669P.
2000US-00711216.
2000US-0248325P.
                                            2000US-0248893P.
2000US-0257511P.
2001US-0260166P.
                                                               2001US-00797039.
2001US-00845044.
                                                                            2001US-00909743.
2001US-00920346.
                                                                                         2001US-00928531.
2001US-00929218.
2001US-0312539P.
                                                                                                                                                                                                              Curtis RAJ, Olandt PJ, Tsai
Silos-Santiago I, Bandaru R;
                   2000US-0235035P.
                                                                                                             2001US-00963159
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                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                             03-JAN-2003; 2003US-00336153
                                                                                                                                                                                                        Kapeller-Libermann R,
                                                                                                                                                                                                                                 WPI; 2004-268788/25.
P-PSDB; ADL14161.
                 25-SEP-2000; 208-NOV-2000; 209-NOV-2000; 214-NOV-2000; 22-DEC-2000; 22-DEC-2000; 25-JAN-2001; 2
                                                                                         13-AUG-2001;
14-AUG-2001;
15-AUG-2001;
                                                                                                                         13-NOV-2001;
15-NOV-2001;
30-JAN-2002;
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22-OCT-2002;
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27-APR-2001;
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31-JUL-2001;
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                                                                                                                   08-NOV-2001;
                                                                                                                                            25-MAR-2002;
12-APR-2002;
                                                                                                                                                                      02-JAN-2003;
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Rudolph-Owen LA; Chun M, Williamson MJ; Meyers RE, Galvin KM, ξ, F,

New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26175, 25643, 26638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.

The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 21967, 11993, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, 14989, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, 14989, angles, 38555 or 539 andelec acid molecules and any one of 40 nuclectide sequences (I). The nucleic acid molecules and confidence, or a subject a trisk of developing a disorder, which is a subject a trisk of developing a disorder, which is a subject a trisk of developing a disorder, which is a subject a trisk of developing a disorder, which is a subject a trisk of developing a disorder, which is a subject a trisk of developing a disorder, which is a subject a trisk of developing a disorders, brain disorders, platelet disorders, breast disorders, platelet disorders, breast disorders, platelet disorders, breast disorders, platelet disorders, conditional disorders, thyroid disorders, thyroid disorders, thyroid disorders, thyroid disorders, skeletal muscle disorders, conducted disorders, skeletal muscle disorders, conducted disorders, disorders, disorders, disorders, disorders, disorders, disorders, disorders, disorders, disorders, disorders, disorders, disorders, neurological or central nervous system conducted disorders, neurological or central nervous system disorders, erythroid disorders, neurological or central nervous system disorders, erythroid disorders, neurological or central nervous system disorders, erythroid disorders, neurological or central nervous system disorders, polypeptides are also useful as modulating agents in regulating a variety of cellular process, e.g. cell proliferation, differentiation, growth and division. This sequence encodes a novel human protein of the invention. Note: The sequence given in the specification are also avaitable in central nervous conduction of the service of the services of the sequence of the services of the sequence of the services of the sequence of the services of the sequence of the services of the sequence of the services of the sequence of the services of ftp.seqdata.uspto.gov/sequence.html?DocID=20040058355

1041 TGTTGATGATGAACCCCACCGCCGGCCACCTGGAGGATGTGGCCAGTCACTGGTGGG 1063 944 GCAACGGGGCCTACCGGGAGCCACCTAAACCCTCTGATGCCTGTGGCCTGATCCGGTGGC 141 441 741 823 883 921 981 CTACTGATTCCCCTGCCGCCCTTGCTCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTCG 175 201 223 261 283 321 343 381 501 561 621 643 703 763 GCAAGTTCCTCCAGACGTTCTGTGGGAGCCCTCTACGCCTCGCCTGAGATAGTCAACG 801 861 344 CCTACGGGAAGGTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAA 403 GCAAGATCGTGATCGTCATGGAGTATGCCAGCCGGGGGGACCTTTATGACTACATCAGCG 583 TGCACTACTGCCACCAGAACGGGATCGTTCACCGAGATCTCAAGCTGGAAAACATCCTTC 681 884 IGGIGCAIGGCACCAIGCCCITICAIGGCCAIGACCAIAAGAICCIAGIGAAACAGAICA 943 AGCGGCAGCAGCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCGCCG CTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTAC 644 TGCACTATTGCCATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCT TAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAACCTGTACCACAAG TGGATGCCAATGGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACAAG 142 TCCAGCGCCCGAGCCCAGGCTCCCTCGGCCTTCGCCTCGGCCTCGGAGAGCGCCCGGCCGC TGGCGGACGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC 224 TGGCGGAAGGGCTGATCAAGTCGCCCAAGCCCCTAATGAAGAAGCAGGCGGTGAAGGGGG ACCATCACAAACACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCAAAGGGCA accacacaagcacarcegeaccecracgagricerggagaccerggecaaagca CCTACGGGAAGGTGAAGAAGGCACGAGAGAGCTCGGGGCGTCTGGTGGCCCATCAAGTCCA GCAAGATTGTGATTGTCATGGAGTATGCCAGCCGAGGCGATCTGTATGATTACATCAGTG AGCGGCCACGGCTGAGTGAGCGGGACGCCAGGCATTTCTTCCGACAGATCGTGTCTGCCC 764 GCAAGTTCCTGCAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATG GGAAGCCCTATGTGGGCCCAGAGGTGGACAGCTGGTCTCTGGGGCGTTCTCCTGTACATCC GGAAGCCCTACACAGGCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCC TGGTGCATGCCACCATGCCCTTTGACGGGCAGGATCATAAAAACACTGGTGAAGCAAATCA GTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGC TGTTAATGGTGAACCCCACCCGTCGGGCCACTGGAGGATGTAGCCAGTCATTGGTGGG 34; Length 3353; Sequence 3353 BP; 754 A; 1022 C; 879 G; 695 T; 0 U; 3 Other; Indels Score 1379; DB 12; Pred. No. 8.2e-295; 0; Mismatches 335; Query Match 47.5%; Best Local Similarity 81.8%; Matches 1654; Conservative 82 116 176 202 262 284 322 404 502 524 295 584 682 704 742 824 982 1004 382 442 622 802 862 922 X G ò g ð 유 ò 셤 ઠ 셤 à 셤 ò g 8 유 ò 원 8 g ò g ò 셤 δ 셤 ઠે g ઠે g 8 요 ò 8

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                                                                                                                 This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the Oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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   Kawai Y;
T, Koga
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                                                                                                                                                                                                                                                                                                                                                     Sequence 3395 BP; 722 A; 1044 C; 894 G; 735 T; 0 U; 0 Other;
   Ishii S,
S, Otsuki
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   Hayashi K,
K, Kojima
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                   Nagai
Ė,
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Ota T, Nishikawa T, Isoga
Wakamatsu A, Sugiyama T,
                                                WPI; 2004-204755/20.
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                                                                                                   New oligonucleotide
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   TCCAGCGCCCCGAGCCTCCCTCGGCCTCCGCCTCGGAGAGCGCCCCGGCCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from human cDNA libraries which can be used for gene therapy or in vaccines. The polymucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence encodes a polypeptide described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
                                                                                                                               CCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAAGGGAGATGGTGCCCTAGTATGGGGTAG
 GTCTGAAGCGATGGTGGCAGGAATCCT
                 TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG
                                                                                                TGGGGACAGCTGCTTTTCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGG
                                                                                                                                                                   CACTGAGGGTCTGCTCAAAGCTCACCTGAGTGGGAGTAGGCATTGCCCCAG-CCCGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gene; gene therapy; vaccine; disease treatment; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Human cell cycle-associated cDNA from clone DKFZphtes3_7j3
                                                                                                                                                                                                      2092
                                                                                                                                                                                                                         Score 1374.2; DB 5; Length
Pred. No. 9.5e-294;
0; Mismatches 338; Indels
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ilarity 81.6%;
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Best Local Similarity
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Claim 2; SEQ ID NO 639; 918pp; English.

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255 ACCACCACAAGCACAACCTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCA
   Query Match
Best Local Similarity 81.6%;
Matches 1651; Conservative
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            human; PRO; membrane bound protein; membrane bound receptor; cell proliferation; cell migration; cell differentiation;
                                                                                                                                                                                         ADF76964 standard; cDNA; 3443 BP
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26-FEB-2004

RESULT 8
ADF76964
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KW humm
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                                                                                                                                                                                polypeptides, useful for diagnosing and treating an immune disorder, e.g. systemic lupus erythematosus, rheumatoid is, osteoarthritis, juvenile chronic arthritis, thyroiditis
mitogenic factor; survival factor; cytotoxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour;
                                                                                                                                 Schoenfeld JR;
                                                                                                                                 Jackman JK,
                                                                                                                                 Hunte B,
                                                                                                22-FEB-2002; 2002US-0359461P.
                                                                                 21-FEB-2003; 2003WO-US005241
                                                                                                                                 Clark H, H, Wood WI,
                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                         WPI; 2003-721702/68.
                                                                                                                                                                                                          diabetes mellitus.
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                                                WO2003072035-A2.
                                                                                                                                 Bodary SC, Cl
Williams PM,
                                 Homo sapiens
                                                                04-SEP-2003
                                                                                                                                                                                                   arthritis,
                                                                                                                                                                                         related
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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information, crecived from orber cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cytotoxic factors, differentiation factors, curropeptides and hormones) which are received and interpreted by diverse cell receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present

nvention.

141 146 201 194 261 254 321 82 CTACTGCTGCCCGACCCACTCCACCTCGCGGTCCCCGCACCATGGAGTCGGTGGCCTTAC 87 cracrearrecerececerrecreaererecreerecreeredareaerecreerree 147 CGCGGCGCTCCGGCCCCACTCCCTCGGCCGCAGAGCTA------GCCCGGCCGC 202 TGGCGGACGGGCTCATCAAGTCGCCTAAACCTCTGATGAAGAAGCAGGCGGTGAAGCGGC ACCATCACAAACACAACCTGCGGCACCGCTACGAGTTCCTGGAGACGCTGGGCCAAGGGCA 142 TCCAGCGCCCGAGCCAGGCTCCCTCGGCCTCCGCCTCGGCCTCGGAGAGCGCCCGGCCGC 34; Gaps Score 1374.2; DB 10; Length 3443; Pred. No. 9.5e-294; 0; Mismatches 338; Indels 34; ( Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;

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Determining the subtype of leukemia cells and whether a patient sample contains leukemia cells or other cells, useful for treating leukemia, comprises determining the expression profile of a group of markers in a
                                                                                                                                     Disclosure; SEQ ID NO 2508; 2938pp; English.
                                      h T, Schoch C, Kern W,
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The present invention relates to a method (M1) for determining the subtype of leukaemia cells and whether a patient sample contains leukaemia cells. The method comprises determining the expression profile of a group of markers in a patient sample. The method is useful for determining the presence of leukaemia cells, its types or subtypes, and for the preparation of a medicament for treating leukaemia.

Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;

47.4%; Score 1374.2; DB 10; Length 3443; ilarity 81.6%; Pred. No. 9.5e-294; Conservative 0; Mismatches 338; Indels 34; ( Similarity Matches 1651; Query Match Local

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                                                                                                               DB 12; Length 3443;
                                                                                Sequence 3443 BP; 763 A; 1043 C; 896 G; 741 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic solerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anoemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the
                                                  -GTCTGAAGCGATGGTGGCAGGAATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy;
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Wu TD;
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This invention relates to a novel isolated, enriched or purified nucleic acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat diseases or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cytostatic, neuroprotective, immunomodulator and antiinflammatory activities. This polynucleotide sequence is a human kinase DNA sequence of the invention.
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sparing a composition for treating diseases or disorders, e.g., cancer,
neurological, immunological or inflammatory disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the argainine-rich protein-like polypeptides, such as mapping, identifization of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel human arginine-rich protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and
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05-MAR-2002; 2002WO-US005095.
20-AUG-2002; 2002US-00225251.
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(XUEA/) XUE A.
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genetic disorder
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GTGGGGATCCCAAGGAGCAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCTCCATCGCAAAG 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
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                  GCATICICAAACICAAIGGCAAGIICICCCGCACAGCCIIAGAAGGCACIACCCCIAGCA
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Ghosh M;
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Yamazaki V, Chen R, Wang Z,
J D, Drmanac RT;
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Yue AJ, Yang Y, Ma
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P-PSDB; ABP69116.
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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ1206) or their mature procein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The cocoded polypeptides (ABP68902-ABP69849) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating celliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autonimume diseases (multiple sclerosis, clabetes, lupus) genetic disorders, wound, burns, incision, ulcers, liver or lung fibzonsis, infections (bacterial, viral, fungal, parastitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format contractly from WIPO at ftp.wipo.int/pub/published_pot_sequences
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New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.3%; Score 1371.8; DB 6; Length 2043; 82.3%; Pred. No. 2.8e-293; ive 0; Mismatches 317; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2043 BP; 418 A; 659 C; 592 G; 374 T; 0 U; 0 Other;
                                                                                                                                                                  SEQ ID NO 215; 1012pp + Sequence Listing; English.
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Qy         1822 CTGAACGTCTTCCCGAAACCCCACTGAGGGCTCTGTGGACAACCTGAGGGGGC 1881           Db         1784 CTGAACGGTCCCCAGAAGCCCCACTGCGGGGCTGTGTCTGTGGACAACCTCAGGGGC 1843           Qy         1882 TTGAGCAGCTCCCTCAGAAG	AAD26459 standard, CDNA, 3160 BP.  AAD26459 tandard, CDNA, 3160 BP.  AAD26459  E. AAD26459 standard, CDNA, 3160 BP.  AAD26459  E. AAD26459  E. AAD26459  E. AAD26459  E. AAD26459  E. AAD26459  E. Mann kinase PKIN-12 CDNA.  E. E. AAD26459  E. Human kinase PKIN-12 CDNA.  E. E. AAD26459  E. Human kinase PKIN-12 CDNA.  E. E. AAD26459  E. Human kinase PKIN-12 CDNA.  E. E. AAD26409  E. AAD26409  E. E. AAD26409  E. AAD26409	
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	GTGGG GTGGGG GTGGG GTGGG GTGGG GTGGG GTGGG GTGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGG GTGGGGGG GTGGGGGG	
GCAAGTTCCTCCAGACGTTCTGGGGAGCCCTCTTACGCCTCGCCTGAGATAGI	TGTTAATGGTGAACCCCACCGGGGGCCACCTGGAGGATGTAGCCAGTCATTGCTGGGGGGCACCGGGGGGGCACCCGGGGGGGG	
TGTGGGAGCCCTC		
TCCTCCAGACGTTC		
742 GCAAGIT 713 GCAAGIT 802 GGAAGIC 802 GGAAGIC 773 GGAAGIC 773 GGAGIC 862 TGGTGC 862 TGGTGC 862 TGGTGC 863 TGGTGC 893 GCAACGC	982 TGTTAN 953 TGTTGAN 1042 TCAACTC 1103 TCAGTGC 1104 TCAGTGC 1105 CTAGTGC 1105 CTGGA 1122 GCACTGT 1133 TCCTGGA 1140 AGGAGGA 1253 TGGCCA 1253 TGGCCA 1253 TGGCCA 1254 GCCTCA 1374 GCCTCA 1402 ACTCCTC 1522 ACTCCTC 1524 GTGGGGGA 1544 GTGGGGGA 1564 GCATTCT 1607 GCATTCT 1607 GCATTCT 1608 GCATTCT 1708 GCATTCT 1608 GCATTCT 1708 GCATT	
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comprise human kinase polypeptides

Page 184; 197pp; English Claim 5;

The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or condition associated with overexpression of PKIN. The disease or conditions and provided in the disease of disease, adult respiratory distress syndrome, disease, attentosoclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, gout, bronchitis, psoriasis, Reiter's syndrome, costeoarthritis, osteoparely syndrome, voitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, cushing's syndrome, hypothyroidism, cerebral palsy, cataracts; cardio vascular disease, hypothyroidism, cerebral palsy, cataracts; cardio vascular disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Pabry's disease, lung tumours); lipid disorder (fatty liver, Pabry's disease, lung tumours); lipid disorder (fatty liver, Pabry's disease, lung tumours); lipid disorder (fatty liver, Pabry's disease, chronic bronchitis, lung tumours); lipid disorder compound and in gene therapy. The present sequence is human by human. PKIN-12

Sequence 3360 BP; 729 A; 1022 C; 882 G; 727 T; 0 U; 0 Other;

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1105 1225 1285 1516 1161 1221 1281 1401 1641 1041 1101 1286 ACCTCAAGCTGCCAAAGGGCATTCTCAAGAAGAAGGTGTCAGCCTCTGCAGAAGGGGTAC 1345 ---CCCTGCTCCCCAAGAAGGGCATTCTCAAGAAGCCCCGACAGCGGGGGGGTCTCGCTACT 1456 1581 AGGAGGACCCTCAGGAACTCAGACCGGTGCCTGATACTCCAGGGCAGCCTGTCCCTGCTG 1461 GCATTCTCAAACTCAATGGCAAGTTCTCCCGCACAGCCTTAGAAGGCACTACCCCTAGCA 1701 1637 CCTTCGGCTCCCTGGATGAACTCGCCCCACCTCGCCCCTGGCCCGGGCCAGCCGACCCT 1696 865 745 925 985 741 801 861 921 981 1106 TCCTGGAGAATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAA GCATCCTCAAACTCCATGGCAAGTTCTCCCAGACAGCCTTGGAGCTCGCGGCCCCCACCA GCAACGGGGCCTACCGGGAGCCACCTAAACCCTCTGATGCCTGTGGCCTGATCCGGTGGC TGTTGATGGTGAACCCCACCCGCCGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGG CTGGCAGTGACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCC GCACTGTACCTGGGCTGGAGCGGCAACATTCTCTTAAGAAGTCCCGAAAGGAGAATGACA 1226 TGGCCCAGTCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCA GCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAGTCCTCTACCTCGTCAGGGGAGGTAC 1457 ACTCCTCCCCAGCCCCAGTGAATCTGGGGGGGCTCTTGGACGCAGGCGACGTGTTTGTGA TAGATGCCAATGGAAACATCAAGATTGCTGACTTTGGCCTCTCCAAACCTGTACCACAAAG TGGGTGCCAATGGGAATATCAAGATTGCTGACCTTCGGCCTCTCCAACCTCTACCATCAAG GCAAGTTCCTCCAGACGTTCTGTGGGAGCCTCTCTACGCCTCGCCTGAGATAGTCAACG GCAAGTTCCTGCAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATG GGAAGCCCTATGTGGGCCCCAGAGGTGGACAGCTGGTCTCTGGGCGTTCTCCTGTACATCC GGAAGCCCTACACACACACAGACACACACTCCTCCTCGGTGTTCTCCTTCTACATCC TGGTGCATGCCATGCCCTTTGACGGCAGGATCATAAAACACTGGTGAAGCAAATCA TGTTAATGGTGAACCCCACCCGTCGGGCCACACTGGAGGATGTAGCCAGTCATTGGTGGG TCAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGGTGGGCCACC CTAGTGGTGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCCC TCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGCAGCACGTGCCGGGAGGTGGAA TGGCTCAAAATCTGCAAGGTGACCCGGCTGAGGATACCTCTTCGCCCTGGCAAGAGCA 1346 Addaddactercedaagercadececaarecerdeaageceaagecadecreece----1462 TATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGCGTGAATCTGGTTACT ACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATGTTTGTGA GTGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCCTCCTCCACCGCAAGG ccittigeciccordeaccaacidecciccitccaiccideagcccogccoagccocci GTAACGGGGCTTACCGTGAGCCGCCCAAGCCGTCCGATGCCTGTGGCCTGATCCGGTGGC 1642 ( 1577 ( 626 742 989 746 908 998 1042 1102 1046 1162 1222 1282 1342 1402 1400 1522 1582 682 802 862 922 982 926 986 1702 4 y g 8 유 ò a 8 g 8 셤 ò 유 ð 셤 ò g 8 g ò 유 g à 셤 Š d ò g ò 셤 ò g ò à

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wortostatic; cardiant; hypotensive; antianginal; osteopathic;
antiathritic; antirheumatic; neuroprotective; antiinflammatory;
antiathritic; antisthmatic; cardiovascular; virucide; analgesic;
watigosciatic; antiathyroid; cardiovascular; virucide; analgesic;
was an antiporitic; antiathyroid; dermatological; immunomodulator;
cell proliferention disorder; cell differentiation disorder;
watin disorder; platelet disorder; breast disorder; colon disorder;
widney disorder; renal disorder; breast disorder; colon disorder;
whoreate disorder; recrized disorder; spleen disorder;
whyroid disorder; restes disorder; haematopoletic disorder;
whoreatic disorder; skeletal muscle disorder; skin disorder;
whoreatic disorder; cardiovascular disorder;
wendothelial cell disorder; liver disorder; viral disease; pain disorder;
metabolic disorder; neurological disorder;
whoreatic manadory disorder; liver disorder;
whoreatic metabolism disorder; viral disease; pain disorder;
whoreatic metabolism disorder; cardiovascular disorder;
blood vessel disorder; anglogenic disorder;
whypertension; anglina; osteostriticis; rheumatoid arthitis;
whypertension; anglina; osteostriticis; rheumatoid arthitis;
whypertension; anglina; osteostriticis; rheumatoid arthitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACTGAGGGTCTGCTCAAAGCTCACCTGAGTGGAGTAGGCATTGCCCCAG-CCCGGTCAG 1995
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CAGGGCTGTGAGTGAGGACAGCATCCTGTCCTCCGAGTCCTTTGACCAATTGGACTTGC
                                                                                                                                                          CTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTGTCTGTGGACAACCTGAGGGGGC
                                                                                                                                                                                                                                                                                                            TTGAGCAGCCTCCCTCAGAAG-----GTCTGAAGCGATGGTGGCAGGAATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGGGATAGCTGCTTTTCTCTGACAGACTGCCAAGAGGTGACTGCAGCCTACAGACAAG
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cell proliferation; cell differentiation; cell growth; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCTGAGAGGGTTTGCAGAGGAACCCTGGGTCGGATTCCTCC 2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1996 GCTCTCAGATGCAGCTGGTTGCACCCCGAGGGGGAGATGCCTTC 2038
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New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.
                                                                                                                                                                                                                                                                      Rudolph-Owen LA;
Chun M, Williamson MJ;
                                                                                                                                                                                                                                                                      Hunter JJ, Meyers RE,
                                      2000US-0235035P.
2000US-0246669P.
2000US-00711216.
                                                                       2000US-0248893P.
2000US-0257511P.
2001US-0260166P.
2001US-00797039.
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                                                                                                      2001US-00845044.
2001US-00909743.
2001US-00920346.
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2001US-0312539P
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03-JAN-2003; 2003US-00336153
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                                                                                                                                                                                                                                                                       Kapeller-Libermann R,
                                                                                                                                                                                                                                                                                                       WPI; 2004-268788/25.
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                              25-SEP-2000;
25-SEP-2000;
                                               08-NOV-2000;
                                                       09-NOV-2000;
                                                                14-NOV-2000;
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                                                                               22-DEC-2000;
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25-SEP-2001;
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                                                                                                                                                                                                                                                                               Curtis RAJ.
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The invention describes an isolated 21910, 56634, 55053, 2504, 15977, CC 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, CC 21967, M1983, m1983, 33155, or 593 nucleic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, which is associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501, CC 37903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 activity, such as cellular proliferative and/or differentiative disorders, kidney (renal) disorders, breast cdisorders, colon disorders, kidney (renal) disorders, prostate disorders, thyroid disorders, spleen disorders, prostate disorders, thyroid disorders, seletal muscle disorders, cardiopoietic disorders, pancreatic disorders, seletal muscle disorders, skin (dermal) disorders, disorders, cardiovascular disorders, colon disorders, disorders, cardiovascular disorders, colon disorders, disorders, associated with bone metabolism, immune, e.g. inflammatory disorders, cardiovascular, viral disorders, metabolic disorders, blood vessel disorders or angiogenic cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardiovascular, cardio

990S-00365162 990S-00392189 990S-00412210. 990S-00448076. 2000US-0186061P.

09-SEP-1999; 05-OCT-1999; 23-NOV-1999; 29-FEB-2000;

98US-00163821. 99US-0117580P. 99US-00276400.

27-JAN-1999, 25-MAR-1999, 30-SEP-1998

25-APR-2003; 2003US-00423543

25-MAR-2004

Claim 1; SEQ ID NO 45; 139pp; English.

A45-04 7733

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                                                                                                                                                              AGGATCTGCTGCACATACGGAGGAGATTGAGATCATGTCTTCACTCAACCACCCCCACA 468
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                                                                                  AACCTCTGATGAAGAAGCAGGCGGTGAAGCGGCACCATCACAAACACAACTGCGGCACC
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                                                                                                                                    AGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAGATGAGC
                                             Gaps
                               12; Length 1884;
                                            21;
                  Sequence 1884 BP; 403 A; 599 C; 548 G; 334 T; 0 U; 0 Other;
                               Query Match
46.9%; Score 1360.2; DB 12; Length
Best Local Similarity 84.2%; Pred. No. 9.9e-291;
Matches 1565; Conservative 0; Mismatches 273; Indels
      ftp.segdata.uspto.gov/sequence.html?DocID=20040058355
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1368 1465 1668 1728 1788 1608 1645 -----GICTGAAGCGATGGTGGCAGGAATCCTTGGGGGATAGCTGCTTTTCTCTGACAG 1956 1234 GAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTTTCCCTGACAG 1825 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGC 2015 CCCAGACAGCTTAGAGCTCGCGGCCCCCACCATCGGCTCCCTGGATGAACTCGCCC TGGCTGACTGGCCTCCGGCGTTCCTCCGCCCCTCCTGGAGAATGGGGCCAAGGTGTGCA CTGAGGATACCTCTCTCGCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCA CTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCCAAGCTGCCAAAGGGCATTCTCA CCCGCACAGCCTTAGAAGGCACTACCCCTAGCACCTTTGGCTCCCTGGACCAACTGGCCT GCTTCTTCAAGCAGGAGGTGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGCCAAC TGGCGGACTGGTTACGTCGCTCCTCGCGCCCCCTGGAGAATGGAGCCAAGGTGTGCA 1766 995 1189 1055 1249 1115 1309 1175 1369 1235 1549 1406 1609 1466 1669 1729 1789 1646 1849 1706

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Match	Match	first
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Description	AK004737	AK033672	AK034082	AY399041	AY399039	AY399040	BI653092	CA319312	CF729223	BG915967	CF726196	CB248251	CO424322	C0041415	CF584809	BI143828	C0041178	BF785290	BB625283	CK781308	BG174288	BG694881	BF789245	BI143493
SUMMARIES ID	AK004737	AK033672	AK034082	AY399041	AY399039	AY399040	BI653092	CA319312	CF72923	BG915967	CF726196	CB248251	CO424322	C0041415	CF584809	BI143828	C0041178	BF785290	BB625283	CK781308	BG174288	BG694881	BF789245	BI143493
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## ALIGNMENTS

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

<sup>32822875</sup> seqs, 18219865908 residues Searched:

<sup>65645750</sup> Total number of hits satisfying chosen parameters:

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Gaps

150

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121

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601 690 661 750 810

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TITLE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 AGGTGAAGAAGGCACGAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAAGAAAG
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Pred. No. 0;
0; Mismatches
                                                         /note="putative"
                                                                                            2899
/note="putative"
                                                                                                                                                                                                                                                          98.8%;
Best Local Similarity 99.9%;
Matches 2867; Conservative
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weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE
KIAA0537 (BC 2.7.1.-) [Homo sapiens] (SWISSPROT|060285,
evidence: FASTY, 56.8%ID, 98.6%length, match=1849)"
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REIEIMSSLARPHIALHEVERSSKYVIVMSYASRGDLYDYTSERPRLSERDARHF
RQIVSALHYPHIALHEVERSSKYVIVMSYASRGDLYDYTSERPRLSERDARHF
RQIVSALHYCHQMGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPL
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SMADWLRRSSRPLLENGAKYCSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQ
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Analysis of the mouse transcriptome based on functional annotation
6 60,770 full-length cDNAs
Nature 420, 563-573 (202)
6 (bases 1 to 2899)
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/clone lib="RikEN full-length enriched mouse cDNA library"
/dev_stage="adult"
94. .1989
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    FANTOM Consortium and the RIKEN Genome Exploration Research
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FEATURES

COMMENT

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y 2071 GAACCCTGGGTCGGATTCCTCCAGTGAATAGAGTACATCAAGGCTCTACGTCTGCAGCC 2130 2042 GAACCCTGGGTCGGATTCCTCCAGTGAATAGAGTACATCAAGGCTCTACGTCTGCAGCC 2101	y 2131 TGACTGAACCTGAAAGAGAGAAAATCGCATTGATGTGGAAAGGAATGGGAACCCTTGC 2190	y 2191 TGCCCGAGTGTTATAGTGGGGTGGCCTGAAGGTGCCTACCTCCTTTGTGCCATGAGTGTC 2250	y 2251 ACCCATGACATTCCCACCCTGTTCTCTGGCTGCACCTTCACATAAGTTTCTGTTTCCAT 2310 2222 ACCCATGACATTTCCCACCCTGTTCTCTGGCTGCACCTTCACATAAGTTTCTTTC	y 2311 CAACCACAGGGTTAGAACCCTGACTTCCTGGGAGGTAATGTGTAGTGACTGCCATTATT 2370	y 2371 TAGAGAAAAGCTCTGGTTTCCATCTGCTGCTGCATCTCAAAGACCTGGGAA 2430	2431	y 2491 GATCTCAGAGACTTGAACCTGAAGCTGTTCCTAGTACCCAGATGTGGATGGA	y 2551 TITCTCAGGCCAACGGGACCTAGAATGTGCTGACTTATTTAT	y 2611 TCTGTTTTTGGTTTTGTTTGTTTGTTTTGTTTTTAAGTGAATTTTGCTGCTTT 2670	y 2671 CAATAATGTGAATGCTGTGTTCTGGGGAACTCCACTGTGCCACTGAAGTTTATGTACAGA 2730  [	y 2731 GAAGTATTTGGCAATGATGCCTCTATTCAAGGGGGGTGGGGGCGTTTTCAAATGTAT 2790	2791 GTCTTGAGCACTGTCTGGATTGAGTCTCCAGTCCCTTCACAGGCT 2762 GTCTTGAGCACTGTCTGGATTGAGTCTCCAGTCCCTTCACACGCT	y 2851 CCTCHTCTTCTTGTGGCCAAAAAAAAAAAAAAAAAAAAAA			AKO AKO 'HTC	
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YASPEIVNGKPYVGPEVDSMSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPK TERFORD PSDACGLIRMLLMVNPTRRATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRA SMADWLRRSSRPLLENGAKVGSFFKQHVPGGGSTVPGLERQHSLGHKKSRKENDMAQNLQ
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93. _1988
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                                                                                                                                                                                                                                                      Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ibhii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakguchi,S., Ikegami,T., Kashiwaji,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
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Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
RARAGawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Nature 409, 685-690 (2001)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
High-efficiency full-length cDNA cloning
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/strain="C57BL/63"
/db_xref="FANTOM_DB:9130215K18"
/db_xref="taxon:10090"
/clone="9130215K18"
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98. .2017
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/strain="C57BL/6J"
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Nature 420, 563-573 (2002)

E (Dasses 1 to 2869)

Radachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hangaki,T., Hara,A., Hashizume,W., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imorani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kono,H., Kono,H., Kouda,M., Nawami,Z., Nojima,Y., Kono,H., Kono,H., Kowa,M., Ohsaki,Y., Satich,R., Nomura,K., Numazaki,R., Ohno,M., Ohsaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Tagami,M., Tagawa,A., Takabashi,F., Takaku-Akahira,S., Takada,Y., Tanaka,T., Towaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
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AK034082

2869 bp mRNA linear HTC 03-APR-2004 mus musculus adult male diencephalon cDNA, RIKEN Full-length enriched library, clone:9330154N24 product:weakly similar to PROBABLE SERINE/THREONINE-PROTEIN KINASE KIAA0537 (EC 2.7.1.-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Nature 409, 685-690 (2001)
                                                                                                       Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Direct Submission
Submitted (16-JUJ-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 23-0-0045, Japan (E-mail:genome-res@ggc.riken.jp,
URL:http://genome.gsc.riken.jp, Tel:81-45-503-9222,
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://fantom.gsc.riken.jp/
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ACAAAATCAAAGATGAGCAGGATCTGCTGCAAAAGGGAGGG	ò a	1447 AGCCTGTCCCTGCTGTATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGACAGC 1506
CACTCAACCACCCCACATCATTGCCATCCATGAA	& g	1507 GTGAATCTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCA 1566
TGTTTGAGAATAGCAGCAAGATTGTGATGTCATGGAGTATGCCGAGCCGAGCGATCTGT 54	ò q	1567 GTGATGTTTGTGAGTGGGGACCCCGTGGAGCAGAAGTCTCCACAGGCTTCAGGGCTCC 1626
CCGAC 60	<i>&amp;</i> 8	1627 TCCTCCACCGCAAGGGCATICTCAAACTCAAIGGCAAGTICTCCCGCACAGCCTTAGAAG 1686
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CTCCA 72	& g	1747 GGCCCAGCCGCCCTCAGGGGCTGTGAGTGAGCATCCTGTCCTCCGAGTCCTTTG 1806
3ccrc6c 78	<i>≿</i> 8	1807 ACCAATTGGACTTGCCTGAACGTCTTCCCGAAACCCCACTGAGGGGCTGTGTGTCTGTGG 1866
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CTGTG 96	\$ B	1987 AAGCCCTAGGAATCTGCTCAAAGCTCAGCTGAGGAAGGGAGATGCTGCCCTAGTATGGGG 2046
TGTAG 10        CTAG 10	& 8	2047 TAGGCTCTGAGAGGTTTGCAGAGGAACCCTGGGTCGGATTCCTCCAGTGAATAGAGTAC 2106
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GTGAGGGTGGGCACCCTAGTGGTGACTTTGGCCGGGCCTCCATGGCGAACTGGTTACGTC	S &	2167 GTGGAAAGGAATGGGAACCCTTGCTGCCGAGTGTTATAGTGGGGTGGCCTGAAGGTGCC 2226
GCTCCTCGCGCCCCTCCTGGAGAATGGAGCCAAGGTGTGCAGCTTCTTCAAGCAGCGG 120	à d	2227 TACCTCCTTTGTGCCATGAGTGTCACCCATGACATTTCCCACCTGTTCTCTGGCTGCAC 2286
TGCCGGGGGGGTGGAACACTGGGCTGGAGCGCCAACATTCTCTTAAGAACTCCC 126	\$ <b>9</b>	2287 CTTCACATAAGTTTCTGTTTCCATCAACCACGGGTTAGAACCCTGACTTCCTGGGAGG 2346
GAAAGGAGAATGACATGGCTCAAAATCTGCAAGGTGACCGGCTGAGGATGCTCTTCTC 132	oy Oy	2347 TAATGTGTAGTGACTGCCATTATTTAGAGAGGAACAGCCTCTGGTTTCCATCTCTGCTG 2406
GCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAAGTCCTCTACCT 138	P &	2407 CTGTGCATCTCAAAGACCTGGGAGACTCGGACGGTGTTTGACTTCATCATCTAGAGGGAC 2466
1328 GCCCTGGCAAGAGCAGCCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAGTCCTCTACCT 1385	ò	2467 CAGATGCCCCTGGACCCCATCTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTCCTAGT 2526

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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submitted (16-NOV-2002) Celera Genomics, 45 West Gude Drive, Submitted (16-NOV-2002) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                          ATTTATTTTTTTGTGATTCTCACTTCTGTTTTTTGGTTTTTGTTTTGTTTTTG
                                                                                                        ATTTATTTTTTGTGATTCTCACTTCTGTTTTTTGGTTTTTTGTTTTGTTTTTTT
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CAGATGCCCCTGGACCCCATCTTAGATCTCAGAGACTTGAACCTTGAAGCTGTTCCTAGT
                                        ACCCAGATGTGGATGGATGCTCTGTTTCTCAGGCCAACGGGACCTAGAATGTGCTGACTT
                                                        TTTTTAAGTGAATTTTGCTGCTTTCAATAATGTGAATGCTGTGTTCTGGGGAACTCCACT
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/db_xref="taxon:10090"
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/locus_tag="HCM0091"
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ATGARGACTCGGTGGCCTTACTCCAGCGCCCGAGCCAGGCTCCCTCGGCCTCCGCCCTGGCC
                                                                                                                                                                                                                                                                          243 AAGCAGGCGGTGAAGCGGCACCATCACAAACAACCTGCGGCACCGCTACGAGTTCCTG
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L Science 302 (5652), 1960-1963 (2003)
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L 2 '(bases 1 to 1887)
RS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Feriera,S., Wang,C., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Blancted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
R This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                              43.6%; Score 1264; DB 9; Length 1
78.5%; Pred. No. 7.1e-287;
.ive 0; Mismatches 380; Indels
                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol type="genomic DNA"
/do_xref="taxon:9606"
<1. .>1887
/locus_tag="HCM0091"
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GSS 12-DEC-2003
AY399039.1 GI:39755028 GSSS.
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   CACGTGCCGGGAGGTGGAAGCACTGTACCTGGGCTGGAGCGGCAACATTCTCTTAAGAAG 1140
                                                                                                       TCTCGCCCTGGCAAGAGGCGCTTAAGCTTCCGAAAGGCATTCTCAAGAAAAGGTCCTCT 1260
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1 (bases 1 to 1987)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, White, T.J., Sninsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                               ACCTCGTCAGGGGAGGTACAGGAGGACCCTCAGGAACTCAGACCGGTGCCTGATACTCCA
                                                                                                                                                                                                         GGGCAGCCTGTCCTGTATCCCTGCTCCCAAGGAAAGGCATCCTTAAGAAGTCTCGA
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                                                                                      TCTCGCCCTGGCAAGAGCGTTAAGCTTCCGAAAGGCATTCTCAAGAAAAGTCCTCT
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SOURCE
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AY399040 1887 bp DNA linear GSS 12-DEC-2003
Pan troglodytes HCM0091 gene, VIRTUAL TRANSCRIPT, partial sequence,
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1 (bases 1 to 1814).
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Reritera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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1957 ACTGCCAAGAGGTGACTGCAGCCTACAGACAAGCCCTAGGAATCTGCTCAAAGCTCAGCT
                 1826 ACTGCCAGGAGGTGACAGCGACCTACCGACAGCACTGAGGTCTGCTCAAAGCTCACCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and order them based on alignment.

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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11 (hases 1 to 746)
12 (hac.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbe-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.I.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1866 row: p column: 04
High quality sequence stop: 746.
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/grain="129.557BL/GJ.FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:5341299"
/tissue_type="tumor, gross tissue"
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/lab_host="DH10B"
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DEFINITION ACCESSION VERSION

RESULT 8 CA319312

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/clone lib="NIH Bmap Fub"
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Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarcs
gel: First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXx-Aso vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Amatcmy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
                ESM Muss musculus (INCOSE modata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (Dases 1 to 795)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbe remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

http://mage.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            342
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Pred. No. 1.3e-158;
0; Mismatches 0;
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/mol_type="mRNA"
/strain="C57BL/6"
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/clone="IMAGE:6816569"
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Mus musculus (house mouse)
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Best Local Similarity 96.8
Matches 765; Conservative
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UI-M-HD0-clc-b-24-0-UI.rl NIH BMAP_HD0 Mus musculus cDNA clone
MMGE:30615119 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nin.gov
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
Seq primer: pYX-5.
                 480
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CACGAGAGAGCTCGGGGCGTCTGGTGGCCATCAAGTCCATCAGGAAAGACAAAATCAAAG
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AUTHORS
TITLE
JOURNAL
COMMENT
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RESULT 9 CF729223

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/clone lib="NIH BMAP HD0"
| /clone lib="NIH BMAP HD0"
| Site 2: Not I; The library was constructed according Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarces gel.First strand cDNA was size fractionated on a 1% agarces priner containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I addaptor, digested with NotI and then cloned directionally into pVX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTATYGAAGT. This library was created for the University lows Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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2067 2127 2187 2247 2307 2367 CTCTGACAGACTGCCAAGAGGTGACTGCCTACAGACAAGCCCTAGGAATCTGCTCAA 2007 1828 GTCTTCCCGAAACCCCACTGAGGGGCTGTGTGTCTGTGACAACCTGAGGGGGCTTGAGC 1887 419 479 239 299 359 AGCTCAGCTGAGGAAAGGGAGATGGTGCCCTAGTATAGGGGTAGGCTCTGAGAGGGTTTGCA 300 GCCTGACTGAACCTGAAAGATGAGAAATCGCATTGATGTGGAAAGGAATGGGAACCCT 360 TGCTGCCCGAGTGTTATAGTGGGGTGGCCTGAAGGTGCCTACCTCTTTGTGCCATGAGT 2068 GAGGAACCCTGGGTCGGATTCCTCCAGTGAATAGAGTACATCAAGGGCTCTACGTCTGCA 240 GAGGAACCCTGGGTCGGATTCCTCCAGTGAATAGAGTACATCAAGGGCTCTACGTCTGCA 2128 GCCTGACTGAACCTGAAAGATGAGAGAAATCGCATTGATGTGGAAAGGAATGGGAACCCT 2188 TGCTGCCCGAGTGTTATAGTGGGGTGGCCTGAAGGTGCCTACCTCCTTTGTGCCATGAGT 2248 GTCACCCATGACATTTCCCACCCTGTTCTCTGGCTGCACCTTCACATAAGTTTCTGTTTC 420 GTCACCCATGACATTTCCCACCCTGTTCTCTGGCTGCACCTTCACATAAGTTTCTGTTTC 2308 CATCAACCACCAGGGTTAGAACCCTGACTTCCTGGGAGGTAATGTGTAGTGACTGCCATT 480 CATCAACCACCAGGGTTAGAACCCTGACTTCCTGGGAGGTAATGTGTGTAGTGACTGCCATT ; 24.6%; Score 714; DB 7; Length 727; ilarity 99.6%; Pred. No. 3.4e-157; Conservative 0; Mismatches 2; Indels Best Local Similarity Matches 725; 1948 2008 Query Match

2487

629

PEATURES

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Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 705)

In (bases 1 to 705)

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at thtp://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
                                                                        2349
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UI-M-GZ0-cjp-h-08-0-UI.rl NIH_BMAP_GZ0 Mus musculus cDNA clone IMAGE:30606415 5', mRNA sequence.
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                                                                        ACATAAGTTTCTGTTTCCATCAACCACCAGGGTTAGAACCCTGACTTCCTGGGAGGTA-A
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Mus musculus
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CF726196.1 GI:37600364
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992 bp mRNA linear EST 05-UUN-2001
60815211F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4937647 5',
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 992)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM10871 row: m column: 08
High quality sequence stop: 695.
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Mus musculus
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/db xref="taxon:10090"
/clone="IMAGE:5718428"
/clone="IMAGE:5718428"
/clone="IMAGE:5718428"
/dab_host="mbryol 12.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
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/clone=lb="NNH BMAP FD0"
/note="Organ: brain; Vector: pXX-A8c; Site 1: EcoR I;
Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNa was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-fT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is TGAGAGAGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"
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UI-M-FD0-byi-a-21-0-UI.rl NIH BMAP_FD0 Mus musculus cDNA clone
IMAGE:5718428 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
1 (bases 1 to 726)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/mol_type="mRNA"
/strain="C57BL/6"
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EST.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                        /tissue type="whole eye"
/dev stage="embryo 12.5,13.5,14.5 dpc"
/dev stage="whole eye"
/dev stage="lembryo 12.5,13.5,14.5 dpc"
/dor bost="While BMAP GZO"
/clone lib="Will BMAP GZO"
/note="Organ: Eye; Vector: pXX- Asc; Site l: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RDNA was size fractionated on a 1% agarcse
gel.First strand CDNA was size fractionated on a 1% agarcse
primer containing a Not I site. Double strand CDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatcmy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program cocidinator."
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                                                                                                                                   'organism="Mus musculus"
                                                                                                                                                                                                                                           db_xref="taxon:10090"
/clone="IMAGE:30606415"
                                                                                                                                                                         'mol_type="mRNA"
'strain="C57BL/6"
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Best Local Similarity 100.0%; Pred. No. 2.7e-147;
Matches 672; Conservative 0; Mismatches 0;
                                                                                                 organism="Mus musculus"
                                                                                                                                                                                         xref="taxon:10090"
                                  Location/Qualifiers
                                                                                                    /mol_type="mRNA"
/strain="C57BL/6"
/db_xref-"-
            Seg primer: pYX-5
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UI-M-HUO-cqx-a-14-0-UI.rl NIH BMAP_HUO Mus musculus cDNA clone

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                                                               GTCAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGCTGGGCAC 1100
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Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                    GTCAACTGGGGTTACACCACCGGAGTCGGGGAACAGGAAGCCCTGCGTGAGGTGGGGCAC 180
                                                                                                                                                                                                                      CCTAGEGGEGACTTTGGCCGGGCCTCCATGGCGGACTGGTTACGTCGCTCCTCGCGCCCC 240
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefil.html
This, clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The following repetitive elements were found in this cDNA sequence: 1-75, >POLY A#Simple_repeat (matched compliment) 297-361, cCAAA) m#Simple_repeat
Seq primer: pYX-3
POLYA=Yes.
CTGGTTACTACTCCTCTCCAGAGCCCAGCGAGTCTGGGGAACTCTTAGACGCCAGTGATG 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 716)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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TAG SEQ=None found"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                             C0041415
C0041415.1 GI:48581955
                                                                                               TGTTTGTGAGTG
                                                                                                                       Query Match
Best Local Similarity
Matches 668; Conserva
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KEYWORDS
SOURCE
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CO041415/c
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AUTHORS
TITLE
JOURNAL
COMMENT
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Mus musculus (house mouse)

Exkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Ext. Daniel (1994)

Interitutes of Health, Mammalian Gene Collection (MGC)

Interitutes of Health, Mammalian Gene Collection (MGC)

Interitutes of Health, Mammalian Gene Collection (MGC)

Interitute (1994)

Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, MD 20892

Baldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gerard Gradwohl (PNAS 97 P1607-1611, 2000)

CDNA Library Preparation: Catherine Lee, Endocrine Pancreas
AGENCOURT 8798011 updated NIH MGC_137 Mus musculus cDNA clone CF584809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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2330 CTCCTTTGTGCCATGAGTGTCACCCATGACATTTCCCACCCTGTTCTCTGGCTGCACCTT 2289

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1; Indels

668; Conservative

Page 18

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/done lib= NIH MGC 137"

/note="Organ: pancreas; Vector: pSPORT1; Site 1: Sall;
Site_2: Not1; Library consists of a pool of clones
rearrayed from the following libraries: Melton normalized
mixed mouse pancreas 1 N1-MMS1, Amplified Melton mouse
islets 1 MIS1-A, and Kaesther ngal wt. Clones rearrayed in
the laboratory of K. Kaestner (University of
Pennsylvania). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2166 TGTGGAAAGGAATGGGAACCCTTGCTGCCCGAG-TGTTATAGTGGGGTGGCCTGAAGGTG 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2282
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                                                               can
DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: IRBD13 row: a column: 01
High quality sequence start: 95
High quality sequence stop: 347.
Location/Qualifiers
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ilarity 96.2%; Pred. No. 3.9e-145;
Conservative 0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 709; Conserv
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Adj32125
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Adj96622
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Adj96434
Ade33554
Ade33555
Adg9777
Abb04431
Abb04431
Abb64432
Adb9668

Murine ne Murine ne Human pro Novel pro

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The present sequence is Murine Lymph node Stromal cell kinase I (MLSK-1). This protein is useful for treating a variety of disorders listed in the disclosure of the specification, including autoimmune disorders, allergic reactions, myeloid or lymphoid cell deficiencies, wound healing and tissue repair and replacement, burns, incisions and ulcers, periodontal disease, inflammatory diseases, tumours and bacterial, viral or fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel murine and human kinase nucleic acids useful for treating inflammations, infections, tumors, allergies, autoimmune diseases, and for stimulating or suppressing immune responses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; Lymph node Stromal cell kinase; MLSK-1; autoimmune disorder; wound healing; periodontal disease; inflammatory disease; tumour; infection; allergy.
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Lefebvre

Rosen CF,

Drucker DJ,

WPI; 2002-241747/29.

03-AUG-2000; 2000US-022650P 12-MAR-2001; 2001US-0274613P 28-MAR-2001; 2001CA-02340783

(ONEO-) 1149336 ONTARIO INC.

02-AUG-2001; 2001WO-CA001109

WO200212456-A2

14-FEB-2002

'Serine/threonine kinase

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ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
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The invention relates to an AMPK (AMP-activated protein kinase)-related
kinase designated SNARK polypeptides and polynucleotides. SNARK
(SNIF/AMP-activated protein kinase) is involved in Stress response to
glucose deprivation. The polynucleotides are useful for expressing SNARK
protein in isolated form or as a protein conjugate. Activation of SNARK
protein in isolated form or as a protein conjugate. Activation of SNARK
ctimulates liver CPT-1 thus enhances lipid metabolism in liver cells and
in other cell types such as heart and sheletal muscles, as well as
in other cell types such as heart and sheletal muscles, as well as
increases GLUT-4 and glycogen in muscle. Activation of SNARK is predicted
to have insulin-like effects that would enhance the disposal of glucose
tho muscle and reduce plasma glucose for the treatment of diabetes and
some type of disorders of lipoprotein production leading to increased
levels of cholesterol or triglycerides. SNARK or its variants may be
administered to a subject to treat or prevent a disease associated with
decreased expression of SNARK, such as diabetes. SNARK antibodies are
used to modulate SNARK activity either in vivo for therapeutic purposes.
SNARK antagonists may be administered to increase fuel production,
decrease glucose uptake and increase levels of blood glucose in a patient
suffering from hypoglycaemia. The present sequence is rat SNARK protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMPK (AMP-activated protein kinase)-related kinase, designated SNARk polypeptides and polynuclectides, useful for treating or preventing diabetes, or other disorders of lipoprotein production leading to increased levels of cholesterol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 94pp; English
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Matches 593; Conservative
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63. .89 /note= "Protein kinase ATP-binding region signature"

Location/Qualifiers

Key Binding-site

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Active-site

Domain

Domain

175. 187 //orde= "Serine/threonine protein kinase active-site" //orde= "Serine/threonine kinase catalytic domain" /note= "Serine/threonine kinase catalytic domain"

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        The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length cDness were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a polypeptide encoded by a full length human cDNA of the invention. Note: The sequence data for this patent did format directly from EPO
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                                                                                                                                                                                   Gape
                                                                                                                                                                628;
                                                                                                                                                                4; Length
                                                                                                                                                                                  Indele
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                                                                                                                                                              Ouery Match 85.8%; Score 2824.5; DB 4
Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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T, Koga
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S, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA; cDNA synthesis; oligo-capping
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K, Kojima
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Wakamatsu A, Sugiyama T, Nagai
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2000JP-00118774.
2000JP-00183765.
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genetic manipulation.
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11-JAN-2000;
02-MAY-2000;
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markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-boliferative disorders (cancer), neurodegenerative diseases (Parkinson's or Alzheimer's disease), autoimmune diseases (multiple sclerosis, diabetes, lupus) genetic disorders, myeloid or lymphoid disorders, platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 ASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA 540
                                                                   AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPL 533
                                                                                                                                 ARPSRPSGAVSEDSILSSESFDQLDLPERLPERGCVSVDNLRGLEQPPSEG----LK 596
                                                                                                                                                                                                                                                                                                                                                                                                         Human; genome mapping; gene therapy; food supplement; virus; fungus; eell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; multiple sclerosis; immunomodulator; nootropic; neuroprotective; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide (1) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful fentifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
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Ghosh
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                                                                                                                                                                        RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
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                                                                                                                                                                                                                                                                                                                                                                               Human polypeptide SEQ ID NO 1163.
                                                                                                                                                                                                                                                                                   standard; protein; 628
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                                                                                                                                                                                                                                                                                                                                                                                                                                  from human cDNA libraries which can be used for gene therapy or in vaccines. The polymucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity and to down regulate. This sequence for detecting the presence of polypeptides in samples. This sequence represents a polypeptide described in the disclosure of the invention
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                                                                                                                                                                                                                                                                                                                                           Nucleic acids having the sequences of clones isolated from libraries different human tissues, useful in recombinant DNA methodologies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 628;
                              Human; gene therapy; vaccine; disease treatment; detection
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cell cycle-associated protein from DKFZphtes3_7j3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.8%; Score 2824.5; DB 4
85.7%; Pred. No. 1.9e-239;
ive 26; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 21; Page 943; 1095pp; English.
                                                                                                                                                                                                                                (GEHU-) GERMAN HUMAN GENOME PROJECT
                                                                                                                                                        2000WO-IB001496.
                                                                                                                                                                                     99US-0149499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   duery Match
Best Local Similarity 85.7
Matches 544; Conservative
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                                                                                                                                                                                                                                                                                                            N-PSDB; ABX71420
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                                                                                            WO200112659-A2
                                                                                                                                                                                                                                                                                                                                                                                                                         invention
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28-SEP-1999;
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28-MAR-2002

Ното варіепв

Galvin

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(MILL-) MILLENNIUM

WPI; 2002-352007/38. N-PSDB; ABK14000.

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|MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                               11;
                                                                                                85.8%; Score 2824.5; DB 5; Length 628;
85.7%; Pred. No. 1.9e-239;
ive 26; Mismatches 54; Indels 11;
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Watches 544; Conservative
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The present invention relates to the isolation of a novel human protein
kinase designated 3700, and the polynucleotide sequence encoding it. The
invention also describes the use of a modulator of the activity of
protein kinase (PK) 3700 for making a modulator of pharmaceutical
composition for modulating the ability of a cell to phosphorylate an
enino acid residue of a substrate protein. Modulators of protein kinase
composition for modulating the ability of a cell to phosphorylate an
amino acid residue of a substrate protein. Modulators of protein kinase
composition, tumourigenesis, mitogenesis, transcription of a gene,
angiogenesis, tissue repair, tissue regeneration, establishment or
composition of atherosclerosis, and signalling across the blood-brain
barrier. The polynucleotide and polypeptide molecules for protein kinase
compositioning, diagnosing, preventing, inhibiting, alleviating, or
curing Pk-related disorders and cellular proliferative and/or
curing Pk-related disorders and cellular proliferative and/or
curing excoma, metastatic disorders or leukaemia). The 3700
curing carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700
carcinoma, sarcoma, metastatic disorders or leukaemia). The 3700
cetect a genetic alteration in a 3700 gene, in chromosome mapping, for
tissue typing, in forenaic biology, and as surrogate markers. The present
sequence represents human protein kinase 3700
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                                                                                                                                                                                                                                                                                                                                              Use of modulators of activity of 3700 protein for making medicament f
e.g., modulating protein phosphorylation or cell signaling, or for
treating or preventing cellular proliferative and/or differentiative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Fig 1; 115pp; English
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Human, protein kinase 3700; PK, protein phosphorylation; tumourigenesis; cell signalling, mitogenesis; gene transcription; angiogenesis; sarcoma; tissue repalr; tissue regeneration; atherosclerosis; blood-brain barrier; cell proliferation disorder; cell differentiation disorder; carcinoma; haematopoietic neoplastic disorder; metastatic disorder; leukaemia; cytostatic; antiatherosclerotic; enzyme.

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(first entry)

02-JUL-2002

Human protein kinase 3700.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information received from other cells and the immediate environment. The information is often transmitted by secreted polypeptides (for example mitogenic factors, survival factors, cyctoxic factors, differentiation factors, neuropeptides and hormones) which are received and interpreted by diverse
                                                                               297 VASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel nucleic acids encoding human PRO secreted
                                       HAPGGGSTTPGLERQHSLXKSRKENDMAQSLHSDTADTAHRPGKSNLKLPKGILKKKVS
                                                                                                                           HVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS
                                                                  TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
                                                                                                              ASDVFVSGDPVEOKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA
                                                                                                                                                           ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEG----LK
                                                                                                                                                                         or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis
                                                                                                                                                                                                                                                                                                                                                                                       cell proliferation; cell migration; cell differentiation; mitogenic factor; survival factor; oytcoxxic factor; differentiation factor; neuropeptide; hormone; cell receptor; receptor-ligand interaction; cytostatic; chondrocyte; tumour.
                                                                                                                                                                                                                                                                                                                                                                             membrane bound protein; membrane bound receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jackman JK, Schoenfeld JR;
                                                                                                                                                                                                                                                                                                                                                     Novel human secreted and transmembrane protein SeqID 640.
                                                                                                                                                                                                        631
                                                                                                                                                                                                                    RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; SEQ ID NO 640; 918pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hunte B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-2002; 2002US-0359461P.
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                                                                                                                                                                                                                                                                                  ADF76965 standard; protein;
                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clark H, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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Williams PM,
                                                                                                                                                                                                                                                                                                                                26-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                             human; PRO;
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cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins, along with the CDNA sequences encoding them. The novel proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present sequence is the amino acid sequence of a human PRO protein of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VASHWWVNWGYTTGVGEQEALREGGHPSCDFGRASMADWLRRSSRPLLENGAKVCSFFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLLENGAKVCSFFKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 HAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRL
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 MESVALLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 GVLYILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS
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                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7%; Pred. No. 1.9e-239;
Matches 544; Conservative 26; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 628
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                                                                                                                                                                                                                                                                                                Sequence 628 AA;
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                                                                                                                                                                                                                                                      invention.
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ADL30886
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Human protein encoded by a full length cDNA clone SeqID 2919.

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The present invention relates to human Adenosine Monophosphate activated Protein Kinase (AMPK)-related kinase 5 (ARK5/ KIAA0537) and its coding sequence, which are useful for imparting stress resistance to cells. ARK5 is useful for treatment and prevention of tumours, nervous disorders, muscle disorders and ataxia teleangiectasia. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agent for imparting stress resistance to cells, comprises DNA encoding for adenosine monophosphate activated protein kinase-related kinase 5 ftreatment of tumors, muscle and nervous disorders, and ataxia
                                                                                  AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHKHNLRHRYEFL
                       ASDVFVSGDPVEQKSPQASGLLLHRKG1LKLNGKFSRTALEGTTPSTFGSLDQLASSHPA
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                                                                                                                                               TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; Neuroprotective; Nootropic; Muscular; Gene therapy; defensalme Monophosphate activated Protein Kinase-related Kinase 5; AMK5; AMK4-related Kinase 5; AMK5; ATMA0537; stress resistance; tumour; nervous disorder; muscie disorder; ataxia teleangiectasia; SNARK
                                                                                                                                  ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEG-
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85.7%; Pred. No. 1.9e-239;
iive 26; Mismatches 54;
                                                                                                                                                                                                                RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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(PHAR-) ORG PHARM SAFETY & RES.
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                                                                                                                                                                                                                                                                                                               standard; protein;
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Best Local Similarity
Matches 544; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               Human SNARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polypeptide sequence is a full length human protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
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human; medicine; signal transduction; glycoprotein; transcription; oligo-capping method.
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T, Koga
                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotide primers (830 cDNAs) useful for synthesizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.8%; Score 2824.5; DB. 8; Length 628;
85.7%; Pred. No. 1.9e-239;
ive 26; Mismatches 54; Indels 11;
                                                                                                                                                                                                                                                                                              Ishii S,
S, Otsuki
                                                                                                                                                                                                                                                                                            Hayashi K,
K, Kojima 8
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                                                                                                                                                                                                                                                                                            Isogai T,
a T, Nagai
                                                                                                                                                                                                                                                            (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                           11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
                                                                                                                                              07-JUL-2000; 2003EP-00025638
                                                                                                                                                                                                                                                                                         Ota T, Nishikawa T, Isog:
Wakamatsu A, Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                           WPI; 2004-204755/20.
N-PSDB; ADL30885.
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                                                                                                                                                                                                                                                                                                                                                                                                            length human cDNAs
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Matches 544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 ARASRPSGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEEPPSEGPGSCLR 593
                  ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory disorder; cardiovascular disorder; disease; pain disorder; metabolic disorder; liver disorder; viral disease; pain disorder; metabolic disorder; neurological disorder; sorder; central nervous system disorder; erythroid disorder; blood vessel disorder; angiogenic disorder; cancer; heart failure; hypertension; angina; osteoarthritis; rheumatoid arthritis; multiple solerosis; Crohn's disease; psoriasis; asthma; cell division; cell proliferation; cell differentiation; cell growth; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic, cardiant, hypotensive, antianginal; osteopathic, antiarthritic; antirheumatic; neuroprotective; antiaflammatory; antiarthritic; antiarthmatic; cardiovascular; virucide, analgesic; cNS; angiogenesis inhibitor; angiogenesis stimulator; cerebroprotective; nephrotropic; antithyroid; dermatological; immunomodulator; cell proliferation disorder; cell differentiation disorder; brain disorder; platelet disorder; breast disorder; colon disorder; kidney disorder; renal disorder; breast disorder; colon disorder; thypoteste disorder; in disorder; platelet disorder; platelet disorder; pancreatic disorder; skeletal muscle disorder; skeletal muscle disorder; skeletal muscle disorder; skin disorder; dermal disorder; bone metabolism disorder; immune disorder;
                                                                                                                                                         KLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSL
                                                                    EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL
                                                                                                                                     KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
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The invention describes an isolated 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 2643, 56638, 18610, 33217, 1967, h1983, m1982, as ancletic acid molecule (I) comprising any one of 40 nucleotide sequences (I). The nucleic acid molecules and polypeptides are useful for diagnosing and treating a subject having a disorder, or a subject at risk of developing a disorder, which is associated with aberrant 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 28343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 activity, such as cellular proliferative and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New 21910, 56634, 55053, 2504, 15977, 14760, 25501, 17903, 3700, 21529, 26176, 26343, 56638, 18610, 33217, 21967, h1983, m1983, 38555 or 593 nucleic acid molecules and proteins, useful for treating, e.g. cancer, heart failure and angina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meyers RE, Rudolph-Owen LA;
Galvin KM, Chun M, Williamson MJ;
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Curtis RAJ, Olandt PJ, Tsai F,
Silos-Santiago I, Bandaru R;
                                                                                                                     99US-0117580P.
99US-00276400.
99US-00395162.
99US-00412210.
99US-00448076.
2000US-0186061P.
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2000US-0234922P.
2000US-0235035P.
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2000US-0257511P.
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2001US-00929218
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2001US-00003690
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N-PSDB; ADL14160, ADL14162.
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23-NOV-1999
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disorders, colon disorders, kidney (renal) disorders, lung disorders, ovarian disorders, kidney (renal) disorders, lung disorders, ovarian disorders, prostate disorders, cervical disorders, spleen disorders, thymus disorders, thymus disorders, thymus disorders, thymus disorders, thymus disorders, shall disorders, disorders, skin (dermal) disorders, disorders, acadiovascular disorders, immune, e.g. inflammatory disorders, varal diseases, pain endothelial cell disorders, liver disorders, viral diseases, pain disorders, endothelial call disorders, neurological or central nervous system disorders, erythroid disorders, blood vessel disorders or angiogenic disorders (all claimed), e.g. cancer, heart failure, hypertension, cascing experience, or asthma. The nucleic acid molecules and polypeptides are also useful as modulating agents in regulating a variety of callular process, e.g. cell proliferation, differentiation, growth and division. This is the amino acid sequence of a novel human protein of the invention. Note: The sequences given in the specification are also every disorders.
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differentiative disorders, brain disorders, platelet disorders, breast
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                                                                                                                                                                                                                                                                                                                                                                                         Length 628;
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                                                                                                                                                                                                                                                                                                                                                                                      85.8%; Score 2824.5; DB 8;
llarity 85.7%; Pred. No. 1.9e-239;
Conservative 26; Mismatches 54;
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Best Local Similarity
Matches 544; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for ing an immune related disorder such as systemic lupus erythematosus, atoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                   rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogram's syndrome, vasculitis, sarchides, autoimmune haemolyvic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central tor peripheral nervous system, demyelinating diseases of the Guillain-Barre syndrome and chronic inflammacory demyelinating polyneuropathy, polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MESVALLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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                                                                                                                                        disorder; systemic lupus erythematosus;
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 628
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ADO20172 standard; protein;
                                                                                                                                      immune related
                                                                                                  Human PRO polypeptide #540
                                                                  (first entry)
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This invention relates to a novel isolated, enriched or purifically, it relates to acid molecule that encodes a kinase polypeptide. Specifically, it relates to human tyrosine and serine/threonine protein kinases (PTK's and STK's), as well as protein kinase-like enzymes. The present invention describes screening methods to identify agonists, antagonists and antibodies that can be used to modulate the activity or function of the mammalian kinase enzymes. As such, these compositions can be used for gene therapy purposes to treat disease or disorders including cancer, immune-related diseases, cardiovascular disease, brain or neuronal associated disease, metabolic and inflammatory disorders. Accordingly, they exhibit cycostatic, neuroprotective, immunomodulator and antiinflammatory acciding activities. This polypeptide sequence is a human kinase protein sequence
                                                                                                                                                                                                                                                                                                                                                                           ETLGKGTYCKVKKARRESSGRLVAIKSIRKDKIKDEQDLMHIRREJEIMSSLNHPHIIAIH
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Pred. No. 2.1e-239;
26; Mismatches 54;
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Best Local Simi:
Matches 544;
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                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule encoding a kinase polypeptide, useful for preparing a composition for treating diseases or disorders, e.g., cancer, or neurological, immunological or inflammatory disorders.
                                                                                                                                                                                                                                                                                                                 AGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPL 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human calcium/calmodulin-dependent protein kinase NuaK2 protein SeqID 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase; human; tyrosine protein kinase; serine/threonine protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTK; STK; gene therapy; cancer; immune-related disease;
cardiovascular disease; brain; neuronal associated disease; metabolic;
inflammatory disorder; cytostatic; neuroprotective; immunomodulator;
antiinflammatory; enzyme; calcium/calmodulin-dependent protein kinase;
                 KLENILLDANGNIKIADFGLSNLYHQGKFLQTFCGSPLYASPEIVNGKPYTGPEVDSWSL
                                                                                                                                                                                        HAPGGGSTTPGLERQHSLKKSRKENDMAQSLHSDTADDTAHRPGKSNLKLPKGILKKKVS
                                                        GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
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N-PSDB; ADJ96554.
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                                   DVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFK
                                                                                                                                                  DVASHWWVNWGYATRVGEQEAPHEGGHPGSDSARASWADWLRRSSRPLLENGAKVCSFFK
                                                                                                                                                                                                                             QHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKS
GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATLE
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Alzheimer's disease; neurodegenerative disorde;
hyperproliferative disorder; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related disease and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity include rheumatoid arbitis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclarosis, asthma, osteoarthritis, disease; cancers and reproductive
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                                                                       Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers
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                    protein kinase,
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                                                                                                                                                                                                                                                                  1 MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 56
the expression of MARK3 in cells or tissues, treating an animal having can suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative discorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
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85.2%; Pred. No. 2.8e-237;
ive 26; Mismatches 56;
                                                                                                                                                                                                       Conservative
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Human; kinase; PKIN-12; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
                AAE16266 standard; protein; 594
                                                                                                           Human kinase PKIN-12 protein.
                                                                            (first entry)
                                                                            26-MAR-2002
                                             AAE16266;
AAE16266
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allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy. /note= "Eukaryotic protein kinase domain" 23. .260 /label= Protein\_kinase\_domain 24. .260 /label= Protein\_kinase\_domain /label= Protein\_kinase\_domain Location/Qualifiers 2000US-0212073F. 2000US-0213467F. 2000US-0215651F. 2000US-0216605F. 14-JUN-2001; 2001WO-US019444 2000US-0218372P 2000US-0228056P .260 WO200196547-A2 Homo sapiens 15-JUN-2000; 23-JUN-2000; 25-AUG-2000; 30-JUN-2000; 07-JUL-2000; 13-JUL-2000 20-DEC-2001 Domain Domain Domain Domain Key 

Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
Gandhi AR, Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald SR;
Ramkumar J, Griffin JA, Kearney L. Burford N, Nguyen DB, Tang YT;
Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;
Lo TP, Khan F, Recipon SA, Atimzai Y, Policky JL, Ding L;
Grether M, Elliott VS, Thangavelu K, Batra S, Ison CH;

(INCY-) INCYTE GENOMICS INC.

WPI; 2002-090207/12. N-PSDB; AAD26459.

New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and diseases such as cancer, comprise human kinase polypeptides.

English Claim 1; Page 152-153; 197pp; The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leuksemia, adenocarcinoma, lymphoma, melanoma, allergies, adult respiratory distress syndrome, atterosolerosis, postorias, gondopatores, gondopature's syndrome, Graves' disease, creamatoid arthritis, slogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, repartits, cusening's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio vascular disease (arteriovenous fiscula, hypertension, vasculitis, isohaemic heart disease, chronic bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, hypochity, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity

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                                                                                                                                                                              DACGLIRWLLMVNPTRRATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMAD 338
                                                                                                                                                                                                               TSSRPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKK 458
                                                                      VSVDNIRGLEQPPSEG----LKRWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
of a test compound and in gene therapy. The present sequence is human {\rm PKIN}{-}12 protein
                                                         7; Gaps
                                       Query Match
82.6%; Score 2720.5; DB 5; Length 594;
Best Local Similarity 87.3%; Pred. No. 2.6e-230;
Matches 521; Conservative 22; Mismatches 47; Indels 7;
                         Sequence 594 AA;
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TYPE: PRT
ORGANISM: Mus musculus
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Sequence 11, Application US/09579664B
Fatent No. 6514719
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Immunex Corporation
APPLICANT: Martin, Unja
APPLICANT: Martin, Unja
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APPLICANT: Martin, Unja
APPLICANT: Maderson, Dirk M.
TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFRENCE: 2923-46
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOCTWARE: PatentIn version 3.1
SEQ ID NO 11
SEQ ID NO 11
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; Pred. No. 2.2e-277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38, Application US/10355975A

Patent No. 675923

GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Bird, Timothy A.
APPLICANT: Martin, Unja
APPLICANT: Anderson, Dirk M.
TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
FILE REFERENCE: 2923-BB
CURRENT APPLICANT: NUMBER: US/10/355,975A

CURRENT APPLICANT: NUMBER: US/10/355,975A

CURRENT APPLICANTON NUMBER: US/10/355,975A

CURRENT APPLICANTON NUMBER: US/10/355,975A

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 38

SOFTWARE: Patentin version 3.1
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Best Local Similarity 99.8
Matches 630; Conservative
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HVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS 420
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                                                                                                                                       TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
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| Fatent No. 675923
| GENERAL INFORMATION:
| APPLICANT: Immunex Corporation
| APPLICANT: Immunex Corporation
| APPLICANT: Immunex Corporation
| APPLICANT: Wired, G. Duke
| APPLICANT: Marchin, Unja
| APPLICANT: Anderson, Dirk M.
| TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
| FILE REPERENCE: 2923-B
| CURRENT APPLICATION NUMBER: US/10/355,975A
| CURRENT APPLICATION NUMBER: US/10/355,975A
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 11 DNOS: 38
| SOFTWARE: PatentIn version 3.1
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100.0%; Pred. No. 2.2e-277;
ive 0; Mismatches 0;
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Qy 481 ASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA 540	· · · · · · · · · · · · · · · · · · ·	ò a	295 RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGPFGRASMADWLRRSSRPLLENGAKV 354 295 RGTLEQIMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMV 336
Qy 541 ARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGCVSVDNLRGLEQPPSEGLKRWWQ 600 		è 8	355 CSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLP 411 1
Qy 601 ESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631		දු පු	412 KGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGIL 456 (2015) 2015 (2015) 20
RESULT 4 US-08-677-298-2		ç qa	457 KKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQ 497 
; Sequence 2, Application us/080/7298; Patent No. 5863729; GENERAL INFORMATION:		oy Q	498 ASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPAA 541 
; TITLE OF INVENTION: BUA SEQUENCES ENCODING HUMAN TCAK-1; TITLE OF INVENTION: KINASE; NUMBER OF SEQUENCES: 17		ð í	RPSRPSGAVSEDS
; COKKESPONDENCE ADDRESS: ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C. ; STREET: 5370 Manhattan Circle, Suite 201		<b>Q</b>	549 TPDRIKFPKGIASKSI 564
CITY: Boulder; STATE: COUNTRY: USA		RESULT 5 US-09-523-849-33 ; Sequence 33, A	-849-33 e 33. Application US/09523849
303 EAL		; Patent; GENERA	
; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS		, APPLI , APPLI , APPLI	APPLICANT: Bandman, Olga APPLICANT: Molteni, Angela APPLICANT: Magnaghi, Paola
; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/677,298	-	, APPLI ; APPLI ; APPLI	ANT: Bosotti, Roberta NATI: Scacheri, Emanuela 'ANT: Isacchi, Antonella
-1-0 AT		; APPLI ; TITLE ; FILE	APPLICANT: Hodgson, Dave TITLE OF INVENTION: HUMAN NIM1 KINASE FILE REFERENCE: PC-0009 US
NAME: Caruthers, Jennie M. REGISTRATION NUMBER: 34,464 REFERENCE/DOCKET NUMBER: 9-96	-	CURRE CURRE	CURRENT APPLICATION NUMBER: US/09/523,849 CURRENT FILING DATE: 2000-03-13 NUMBER OF SEQ ID NOS: 39
; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (303) 499-8080 ; TELEFAX: (303) 499-8089		SOFTW SEQ ID	
; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS: . TRACTH: 720 amino acide		TYPE: PR ORGANISM	TYPE: PRT OGANIEM: Homo sapiens PRATHIRE.
TYPE: TYPE:		, NAME ; OTHE US-09-52	NAME/KEY: misc feature OTHER INFORMATION: GenBank Accession No. 6458561 g3089349 9-523-849-33
298-2 atch cal Similarity 35.1%; Pred. No. 3.46-52;		Query Match Best Local 8 Matches 199	<pre>iatch</pre>
MACCAGE 195; CONSEIVALIVE /e; MIEMACCAGE 180; INDGES 105; CADE 57 YEFLETLGKGYYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH		& a	57 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 115 
56 YRLLKTIGKGNFAKVKLARHILTGREVAIKIIDKTQL-NPTSLQKLFREVRIMKILNHPN 116 IIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFRQIVSALHYCHQNGI  :::     :::	·	장 : 음	116 IIAIHEVFENSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 175
DD 115 IVKLFEVIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRI 174 QY 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGFEV 235		ò 8	176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 235 
Db 175 VHRDLKAENLLLDADMNIKIADFGFSNEPTVGGKLDTFCGSPPYAAPELFQGKKYDGPEV 234		ć	236 DSWSLGVLLYILVHGTMPPDGQDHKTLVKQISNGAYREPPRPSDAC-GLIRWLLMVNPTR 294

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DVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRVPFYMSTDCENLLKKLLVLNPIK 298
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                                                                                                                                                                                                            : | : | : | : | : | | | 337 GMGYSQE------EIQESLSKOMKYDEITATYLLLGRKSSEVRPSSDLNNSTGQS- 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 ISSRKSTGSAVGCKGIAPASPM--LGNASNPNKADIPERKKSSTV-----PSSNTAS 483
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   235 DVWSLGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIK 294
                                                          RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKV 354
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// NAME/KEY: misc_feature
// OTHER INFORMATION: GenBank Accession No. 6458561 g2052189
US-09-523-849-32
                                                                                                                 RGTLEQIMKDRWINAGH-----BEDELKPFVEPELDISDQKRIDIM-
                                                                                                                                                                                                                                                                                            408 LKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPR-
                                                                                                                                                                        355 CSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNL---
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35.6%; Pred. No. 4.3e-51;
tive 76; Mismatches 189;
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AFFLICANT BOSOTLI, ROBERTA
APPLICANT: Scacheri, Emanuela
APPLICANT: Heacchi, Antonella
APPLICANT: Hodgson, Dave
TILE REFERENCE: PC-0009 US
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT APPLICATION NUMBER: US/09/523,849
CURRENT PLING DATE: 2000-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PERL PROGRAM
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/09523849 Patent No. 6458561
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Best Local Similarity 35.6%
Matches 187; Conservative
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                                                                                                                                                                                                                                                                                                                          KGILKKKKSSTSSGE----VQ---EDPQELRPVPDTPGQPVPAVSLLPRK-----GIL 456
                                                                                                                                                                                                                                                                                                                                                                                                                                        KK---SRQRES-----GYYSSPEPSESGELLDASDVFVSGDPVEQKSPQ 497
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CSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNL---QGDPAEDTSSRPGKSSLKLP 411
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                                                                                     RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKV 354
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Sequence 1022, Application US/09538092

Sequence 1022, Application US/09538092

Sequence 1022, Application US/09538092

Sequence 1022, Application US/09538092

PETER NOTE OF INFORMATION:

APPLICANT: Glot, Loic

APPLICANT: BAREFIELD A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 1596-542

CURRENT APPLICATION NUMBER: US00-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR PLILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1022
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                                                                                                                             FEATURE:

NAME/KEY: misc feature

LOCATION: (0)...(0)

OTHER INFORMATION: Polypeptide Accession Number P27448
US-09-538-092-1022
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Matches 191, Conservative
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OY   355   CSFPKQHVPGGGSTVPGLERQHSLKKSRKENDMA	RESULT 9 US-09-984-890-2  j Sequence 2, Application US/09984890  patent No. 6492156  patent No. 6492156  GENERAL INFORMATION:  APPLICANT: YAN, Chunhua et al.  TITLE OF INVENTION: ACID MULECULES ENCODING HUMAN KINASE PROTEINS, AND USES  TITLE OF INVENTION: THEREOF  TITLE OF INVENTION: THEREOF  TITLE OF INVENTION: THEREOF  TITLE OF INVENTION: THEREOF  CURRENT APPLICATION NUMBER: US/09/984,890  CURRENT APPLICATION NUMBER: US/09/984,890  CURRENT FILING DATE: 2001-10-31  NUMBER OF SEQ ID NOS: 4  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 2  LENGTH: 74  TYPE: PAT  CRANISM: Homo sapiens  US-09-984-890-2	Query Match         20.6\$; Score 680; DB 4; Length 724;           Best Local Similarity 32.0\$; Pred. No. 3.7e-50;           Matches 201; Conservative 99; Mismatches 195; Indels 134; Gaps 25;           Qy         6 LLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 60             :   :   :	61 ETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI :	DD 116 FEVIETEKTLYLVMEYASGGEVFDYLVAHGRMKEKEARAKFRQVVSAVQYCHQKFIVHKD 175  QY 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239	OY 240 LGVLLVILVHGTMPPDQDDHKTLVKQISNGAYREPRKPSDAC-GLIRWLLMVNPTRRATL 298	359 KQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAED-TSS :::
QY         295         RATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLE-NGAK 353           Db         299         RGSLEQIMKDRWMNVGHEBEBLKFYSEPELDLNDAKRIDIMVTMGFARDEINDAL 353           QY         354         VCSFFKQ	RESULT 8  US-09-523-849-36  US-09-523-849-36  Sequence 36, Application US/09523849  Patent No. 6458561  GENERAL INVEWATION:  APPLICANT: Bandman, Olga  APPLICANT: Magnaghi, Paola  APPLICANT: Bosotti, Roberta  APPLICANT: Bosotti, Roberta  APPLICANT: Isacchi, Antonella  APPLICANT: Padgaon, Dave  TILE REFERENCE: PC-0009 US  CURRENT APPLICATION: HUMAN NIMI KINASE  FILE REFERENCE: PC-0009 US  CURRENT APPLICATION NUMBER: US/09/523,849  CURRENT FILING DATE: 2000-03-13  NUMBER OF SEQ ID NOS: 39	; SEQ ID NO 36; ; TENCTH: 745; ; OVEANISM: Homo sapiens ; FEATURE: ; NAME/KEY: misc_feature ; OTHER INFORMATION: GenBank Accession No. 6458561 g1749794	Query Match 20.9%; Score 688; DB 4; Length 745;  Best Local Similarity 32.9%; Pred. No. 7.8e-51;  Matches 185; Conservative 89; Mismatches 192; Indels 96; Gaps  57 YEPLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLHIRREIEIMSSLNHPH	DD 20 YKLLKTIGKGNFAKVKLARHILTGKEVAVKIIDKTQL-NSSSLQKLFREVRIMKVLNHPN 78 QY 116 IIAIHEVFENSSKIVIVMEYAGRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGI 175	OY 176 VHRDLKLENIILDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV 235	295 RATLEDVASHWWYNWGYTTGVGEQEALREGGHPSGDFGRASWADWLRRSSRPLLENGAKV

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Qy	RESULT 11 US-09-980-4 ; Sequence 4, Application US/09984890 ; Sequence 4, Application US/09984890 ; Patent No. 6492156 ; GENERAL INCOMMATION: ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES ; TITLE OF INVENTION: THEREOF ; FILE REPERENCE: CL001306 ; CURRENT APPLICATION NUMBER: US/09/984,890 ; CURRENT PALICATION NUMBER: US/09/984,890 ; CURRENT PALICATION NUMBER: US/09/984,890 ; SEQ ID NOS: 4 001-10-31 ; NUMBER OF SEQ ID NOS: 4 001-10-31 ; SEQ ID NO 4 ; LENGTH: 722 ; TYPEP PRT ; ORCANISM: Rattus norvegicus US-09-984-890-4	Query Match 20.6%; Score 677.5; DB 4; Length 722; Best Local Similarity 32.9%; Pred. No. 6.1e-50; Matches 201; Conservative 92; Mismatches 203; Indels 115; Gaps 24;	OY 6 LLORPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 60   1   1   1   1   1   1   1   1   1	Oy 61 ETLCKGTYCKVKKARE-SSGRLVAIKSIRKDEQDLLHIRREIEIMSSLNHPHIIAI 119	OY 120 HEVPENSSKIVIVMEYASRGDLYDYISERPRLSERDARHPFRQIVSALHYCHQNGIVHRD 179  116 FEVIETEKTLYLVMEYASGGEVFDYLVAHGRMKEKEARARFRQIVSAVQYCHQKFIVHRD 175	OY 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSFLYASPEIVNGKPYVGPEVDSWS 239	Oy 240 LGVLLYILVHGTMPPDGQDHKTLVKQISNGAYREPFKPSDAC-GLIRWLLMVNPTRRATL 298	OY 299 EDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358	Oy 359 KQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAED-TS 400	Qy 401 SRPGKSSLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSR 460	Qy 461 QRESGYXSSPEPSESGELLDASDVFVSGDP-VEQKSPQASGLLL 503
Qy         402 RPGKSSLKLPKGI		; IENGTH: 724 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-274-194-2	Query Match Best Local Similarity 32.0%; Pred. No. 3.7e-50; Matches 201; Conservative 99; Mismatches 195; Indels 134; Gaps 25;	Qy 6 LLQRPSQAPSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL 60   1   1   1   1   1   1   1   1   1	OY 61 ETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI 119 	QY 120 HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFRQIVSALHYCHQNGIVHRD 179	QY 180 LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239 Db 176 LKAENLLLDADMNIKIADFGFSNEFTFGNKLDTFCGSPPYAAPELFQGKKYDGPEVDVWS 235	QY 240 LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298  Db 136 LGVILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKKFLILNPSKRGTL 295	QY 299 EDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358	QY 359 KQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAED-TSS 401	QY 402 RPGKSSLKLPKGI

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57 YEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPH 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 KRGSLEQIMKDRWMNVGH-----BEEELKPYSEPELDLNDAKRIDIMVTWGPARDEINDA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSWSLGVLLY1LVHGTMPFDGQDHKTL-VKQISNGAYREPPKPSDAC-GLIRWLLMVNPT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 RRATLEDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLE-NGA 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 779;
                                                                                                                                                                                                                                                                                                             & Borun
                                                                                                                                                                                                                APPLICANT: MANDELKOW, Eckhard, et al.
TITLE OF INVENTION: No. 6579691el Protein Kinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray
STREET: 233 S. Wacker Drive, 6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.5%; Score 675; DB 4; L. 35.4%; Pred. No. 1.1e-49; ive 75; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP95/04258
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 94 11 7122.5
FILING DATE: 28-OCT-1994
INFORMATION FOR SEQ ID NO: 31:
LENGTH: 779 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/817,832B
FILING DATE: 28-APR-1997
                                                                                                                                                     Sequence 31, Application US/08817832B
Patent No. 6579691
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.49
Matches 186; Conservative
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    559 --ESFDQLDLP 567
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                                           545 LROVRDÓQNLP
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STRANDEDNESS: si
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                            KINASE PROTEINS, NUCLEIC
ENCODING HUMAN KINASE PROTEINS, AND USES
                           116 FEVIETEKTLYLVMEYASGGEVFDYLVAHGRMKEKERARAKFRQIVSAVQYCHQKFIVHRD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QRESGYYSSPEPSESGELLDASDVFVSGDP-VEQK----SPQASGL------LL, 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 DRASLGQASIQNGKDS-TAPQ-RVPVASPSAHNISSSSGAPDRINFPRGVSSRSTFHAGO 544
504 HRKGILKL---NGKFSRTALEGTTPSTFGSLDQLASSHPAA-RPSRPSGAVSEDSILSS- 558
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                                                                                                                                                                                                                                                                           GENERAL INCORNATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTITUE OF INVENTION: ACID MOLECULES ENCODING TITLE OF INVENTION: THEREOF FILE REFERENCE: CL001306DIV CURRENT APPLICATION NUMBER: US/10/274,194; CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                  US-10-274-194-4
; Sequence 4, Application US/10274194
; Patent No. 6706511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Rattus norvegicus
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                                                                                                            545 LROVRDOONLP 555
                                                                                      --ESFDQLDLP 567
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Best Local S
Matches 201
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QY	Db 356 ATYLLLGYKSSELEGDTITLKPRPSADLTNSSAPSPSHKVQRSVSANPKQR-R 407  Qy 364 GGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKS 419  Db 400 SCHANVDA PDRONY SEKTONDA 1	420STSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSS 420STSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSS	OY 470	Db 553 NLPFGVTPASPSGHSQGRRG-PSGSIFSKFTSKFVRNLNEPESKDR 598  Qy 581 VDNLR 585	Db 599 VETLR 603	RESULT 15 US-09-523-849-35 ; Sequence 35, Application US/09523849 ; Patent No. 6458561 ; GENERAL INFORMATION:	-	; APPLICANT: Basoftl, Roberta ; APPLICANT: Scacheri, Emanuela ; APPLICANT: Isacchi, Antonella ; APPLICANT: Isacchi, Antonella ; TILE REPERENCE: PC-0009 US ; CURRENT APPLICATION NUMBER: US/09/523,849 ; CURRENT FILING DATE: 2000-03-13 ; NUMBER OF SEQ ID NOS: 39	; SOFTWARE: PERL Program ; SEQ ID NO 35 ; LENGTH: 604 ; TYPE: PRT ; ORGANISM: Drosophila melanogaster	; FEATURE: ; NAME/KEY: misc_feature ; OTHER INFORMATION: Genbank Accession No. 6458561 g2564680 ; FEATURE:	; NAMMAKKEY: ungure ; LOCATION: 52, 291, 354 ; OTHER INFORMATION:unknown or other US-09-523-849-35	Query Match 19.8%; Score 653; DB 4; Length 604; Best Local Similarity 33.0%; Pred. No. 6.2e-48; Matches 190; Conservative 76; Mismatches 206; Indels 104; Gaps 19;	Qy 5.7 YEFLETLGKGTYGKVKKA-RESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNH 113	Qy 114 PHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQN 173
394LKVQRTISANQKQRRFSDHAGPSIPPAVSYTKRPQANSV 432 458 KSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQ 497	498 ASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARP 543 		E 2 2 3 2	Chicago E: Illinois IRY: US	AIF: 60608-540Z COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	OPERATING SYSTEM: PC_DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/817,832B FILING DATE: 28-APR-1997	PRIOR APPLICATION DATA: APPLICATION NUMBER: WO PCT/EP95/04258 FILING DATE: 30-0CT-1995	FALOR APPLICATION DATA: APPLICATION NUMBER: EP 94 11 7122.5 FILING DATE: 28-OCT-1994 INFORMATION FOR SEQ ID NO: 32. SEQUENCE CHARACTERISTICS: LENGTH: 722 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear	MOLECULE TYPE: protein 08-817-832B-32 uery Match 20.5%; Score 673.5; DB 4; Length 722; est Local Similarity 31.3%; Pred. No. 1.4e-49;	18; Mismatches 212; Indels 157; Gaps ARPLADGLIKSPKPLMKKQAVKRHHKHNIRHRYEFL		HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFROIVSALHVCHQNGIVHRD 17	LKLENILLDANGNIKIADFGLSNLYHKGKFLQFFCGSPLYASPEIVNGKPYVGFEVDSWS	LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 29

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	234 EVDSWSLGVLLYILVHGTMPPDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNP 292	240 EVDSWSLGVVLYTLVSGSLPFDGTNLKELRDRVLRGKYRVPYYVSIECESLXRKFLVLNP 299	293 TRRATLEDVASHWWVWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGA 352	300 TQRTSLSAVMADRWINMGYEQGNG-LRPFQEKPMDLHDVNRLSLLSNWGHKPRDVXQSLK 358	353 KVCSFFKQHVPGGGSTVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKS 406	359 NQKFDDIYCAYMLLDVAKPRSTACSEKSGSSFRETPTAMPGSS 401	407 SLKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSL 449	402 RIPVPIAAPNVTISQVTFALDKSTPNRPGATSIRPMAPRLANALTPLFLTPP 453	450 LPRKGILKKSRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLL 503	454 -PKKYICCSASKAANPRRSEPSSIPQSAMPKKGVGSPVDVKTTLL 497	504 HRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARP-SRPSGAVSEDSILSSEFD 562	498 SAORKLAVNHKLTSASHQIRSPITQSSQASECTRIPPTHFE 539	563 QLDLPERLPETPLRGCVSVDNLRGLEQPPS-EGLKR 597	540 MLDSTSTPLKVLKLVASNSQTPPSTENINR 569	
QQ	λ̈́O	qi Q	ò	q	δ	qq	ò	q	ò	qq	ò	qq	ò	qq	

Search completed: January 22, 2005, 06:44:54 Job time : 43.6867 secs

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January 22, 2005, 06:29:16; Search time 38.5452 Seconds (without alignments) 1575.104 Million cell updates/sec Run on:

US-09-980-464-11 3293 1 MESVALLQRPSQAPSASALA.......DCQEVTAAYRQALGICSKLS 631 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sv

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		df				
Result No.	Score	Query Match	Length	DB	ID	Description
	888	27.0	1558	7	T29253	hypothetical prote
7	694.5	21.1	713	7	827966	ine/t
м	689	20.9	745	7	G01025	reonine
4	686.5	ö	774	~	148609	probable serine/th
S	699	20.3	1192	~	T18611	
9	667	20.3	1246	~	G89287	I
7	664	20.2	1398	7	T13741	hypothetical prote
α	649.5	19.7	512	~	T52633	ㅁ
6	648.5	19.7	633	П	A26030	serine/threonine-s
10	648	19.7	798	7	JC7500	gik protein - chic
11	641	19.5	504	7	T10449	probable serine/th
12	639.5	19.4	512	Н	JC1446	serine/threonine-s
13	631	19.2	511	Н	A56009	serine/threonine-s
14	630.5	19.1	552	Н	S51025	[hydroxymethylglut
15	627.5	19.1	602	7	S72513	FOG2 protein - yea
16	623.5	18.9	552	н	A53621	[hydroxymethylglut
17	622		562	7	T29858	hypothetical prote
	621	18.9	472	~	B90100	SNF-related kinase
19	620		504	~	T07415	probable serine/th
20	612		481	~	149072	protein kinase - m
	610	•	473	н	S59941	serine/threonine-s
22	669	18.2	512	~	T07788	probable serine/th
	g,	18.1	887	~	T20941	hypothetical prote
	σ	18.1	576	~	T41587	
25	æ	17.8	622	-	844859	serine/threonine-s
26	583.5	17.7	891	~	A38903	protein kinase 1 -
	æ	17.7	891	~	0	protein kinase kin
28	579	17.6	510	7	11	serine/threonine p
	570	17.3	502	Н	A41361	serine/threonine-s

SNF1-related prote	serine/threonine-s	serine/threonine-s	serine/threonine-s	probable protein k	serine/threonine-s	GIN4 protein - yea	p69Eg3 protein - A	probable serine/th	protein kinase KIN	probable serine/th	probable serine/th	probable protein k	hypothetical prote	SNF1-related prote	probable protein k
B90120	860303	\$60304	564930	C84667	S52687	859359	S52244	A86427	\$29344	T14735	T14736	E84707	T33998	S62365	T02306
7	н	٦	7	7	~	7	7	7	7	7	7	~	~	~	0
401	513	513	1147	441	1064	1142	651	480	800	440	440	435	726	746	502
17.3	17.1	17.1	17.0	16.7	16.7	16.6	16.6	16.5	16.5	16.4	16.3	16.2	16.1	16.0	15.9
569.5	564	563	559	549.5	549	547	545	543.5	543	539.5	537.5	534.5	529.5	527	524

## ALIGNMENTS

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123233 hypothetical protein B0496.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #seguence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

Cincession: T29253
R.Murray, J.; Le, T.T.
Submitted to the EMBL Data Library, May 1996
A; Describtion: The sequence of C. elegans cosmid B0496.
A; Reference number: Z20596
A; Recession: T29253
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-1558 wMRA.
A; Residues: 1-1558 wMRA.
A; Residues: 1-1558 wMRA.
A; Residues: EMBL: U58749; PIDN: AAB00636.1; GSPDB: GN00022; CESP: B0496.3
A; Resperimental source: strain Bristol N2; clone B0496
C; Genetics:
A; Reperimental source: strain Bristol N2; clone B0496
A; Reperimental source: strain Bristol N2; clone B0496
A; Reperimental source: strain Bristol N2; clone B0496
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Query Match 27.0%; Score 888; DB 2; Length 1558; Best Local Similarity 37.0%; Pred. No. 2.1e-28; Matches 230; Conservative 73; Mismatches 214; Indels 104; Gaps

54 RHRYEFLETLGKGTYGKVKKARESS-GRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLN 112 g ઠે

113 HPHIIAIHBVFENSSKIVIVMEXASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQ 172 g ò

173 NGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVG 232 ò

셤

233 PEVDSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNP 292 252 PEVDCWSLGILLYTLVYGSMPFDGRDFNRWVRQIKRGAYFEPETPSTASMLIRNMLRVNP 311 ò 유

312 ERRATIFDIASHWWLNLEENMPVIQELPENQIIDHTPLTEREETMIVQDLADEQDVFMEF 371 d à

--SSRPLLENGAKVCSFFKQHVPGGGSTV 369 372 GHLSSETRRKIEDFRIRRKEAEEFNDNSPVKPPKARKTDELTGKISKEQPEEMKSAEKSL 431 GHPSGDFGRASMADWLRR-----325 ð g

370 PGLERQHS------LKKSRK-ENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKK 418 ò 셤

Qy         500 GLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPAARP 543           bb         484 GAMTRNTVCSERTTDDRHSVIQ-NGKENSTIPDQRTPVASTHSISSAATP 534           Qy         544 SRPSGAVSEDS 554           bb         535 DRIRFPRGTASRST 548           RESULT 3         G01025           serine/threonine protein kinase - human         C; Species: Home sapiens (man)           C; Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004           C; Accession: G01025	9	OY 176 VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPVGPEV 235  139 WHRDLKAENLLLDADANNIKIADFGFSNEFFFCKKLDTFCGSPPYAAPELFCGKKYDFEV 198  OY 236 DSWSLGVLLYILVHGTWPPTGQDHKTLVKQISNGAYREPFKBSDG-GLIRMLLMVNPTR 294  139 DVWSLGVLLYILVHGTWPPTGQDHKTLVKQISNGAYREPFKBSDG-GLIRMLLMVNPTR 294  Db 295 RATLEDVASHWWVNMQYTTGVGEQBALREGGHPSGDFGRASMADMLRRSSRPLLENGAKV 354  Db 259 RATLEDVASHWWVNMQYTTGVGEQBALREGGHPSGDFGRASMADMLRRSSRPLLENGAKV 354  Db 259 GTLEDVASHWWVNMQYTTGVGEQBALREGGHPSGDFGRASMADMLRRSSRPLLENGAKV 354  Db 259 GTLEDVASHWWVNMQYTTGVGEQBALREGGHPSGDFGRASMADMLRRSSRPLLENGAKV 359  OY 295 RATLEDVASHWWVNMQYTTGVGEQBALREGGHPSGDFGRASMADMLRRSSRPLLENGSMG
Qy 419 SSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKGRQRESGYYSSPEPSESGEL 478  Db 486 KEKSPEQQPEDPRTARGTSKPADSRAP-SFVPVKDRPETSEPERPRTRPH 534  QY 479 LDASDVFVSGDPVEQKSPQASGILLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLAS 536	erine/threonine- e names: protein Homo sapiens (m. 1-Apr.1993 #son, 527966 mr; \$8.7	### SECTION   STATE

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- Caeno

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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1192 <WILI>
A;Cross-references: UNIPROT: Q9TW45; EMBL: Z81027; PIDN: CAB54179.1; GSPDB:GN00023; CESP:H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 5
A;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 992
C;Keywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific proc
F;1-1192/Product: probable serine/threonine-specific protein kinase, long splice form #8:
F;1-487,536-1192/Product: probable serine/threonine-specific protein kinase, short splic
                                                                                                                                                               splice form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-1192 <#MILJ2 </milder |
A;Cross-references: EMBL:206102; PIDN:CAB54263.1; GSPDB:GN00023; CESP:H39E23.1a
A;Experimental source: clone H39E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-487,536-1192 <WIL4>
A;Cross-references: EMBL:296102; PIDN:CAB54262.1; GSPDB:GN00023; CESP:H39E23.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPDB:GN00023; CESP:H39E23.1b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVH 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRA 296
                                                                                                                                                                                                                                    09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SQAPSASALASESARPLADG------LIKSPKPLMKKQAVKRHHHKHNLRHRYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.3%; Score 669; DB 2; Length 1192; 32.4%; Pred. No. 8.2e-20; tive 97; Mismatches 218; Indels 7
                                                                                                                                                        probable serine/threonine-specific protein kinase (EC 2.7.1.-), N:Contains: probable serine/threonine kinase, short splice form C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text_change C;Accession: T18611; T18610; T23144; T23143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: CAB54178.1;
                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1996
A;Reference number: 218997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;McMurray, A.
submitted to the EMBL Data Library, June
A;Reference number: 219696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Status: translated from GB/EMBL/DDBJ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: CESP: H39E23.1a; CESP: H39E23.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: clone H39E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone AH10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental source: clone AH10 Accession: T18610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-487,536-1192 <WIL2> A; Cross-references: EMBL:281027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 32.48 Matches 187; Conservative
                                            561
                                         RPSTAPORVP
DQLDLPERLP
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562
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                             Cipaces Mus musculus (house mouse)
Cipaces Mus musculus (house mouse)
Cipaces (2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
Cipaces (02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Aug-2004
Cinaces and 148609; Si3133
A; Tiglis, J.D.; Lee, M.; Hill; R.E.
Mamm. Genome 4, 401-403, 1993
A; Title: Emk, a protein kinase with homologs in yeast maps to mouse chromosome 19.
A; Accession: 148609; MUID:93364122; PMID:8358177
A; Accession: 148609; MUID:93364122; PMID:8358177
A; Accession: 148609
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-774 < TING1>
A; Residues: 1-774 < TING1>
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A; Residues: UNIPROT:Q05512; EMBL:X70764; NID:957919; PIDN:CAA50040.1; PID:957926
B; Tinglis, J.D.; Lee, M.; Hill, R.E.
Submitted to the EMBL Data Library, January 1993
A; Description: A novel protein kinase with homologues in yeast maps to mouse chromosome A; Reference number: S31333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPSESGELLDASDVFVSGDP-VEQK----SPQASGL------LLHRKGILKL-- 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMVNPTRRATL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 KOHVPGGGSTVPGL---ERQHSLKKSRKENDMAQNL-----QGDPAEDTSSRPGKSSLKL 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNSSAPSPSHKVQRSVSANPKQRR----SSDQAVPAI---PTSNSYSKKTQSNNAENKRP 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDVASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFF 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     411 PKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSP 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NGKFSRTALEGTTPSTFGSLDQLASSHP-----AARPSRPSGAVSEDSILSSESF 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-699, 'K',700-702,'GRGLPTAAKASCTSGTCYCAGMAHQATRT',731-774 <ING2>
A;Cross-references: BMBL:X70764
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein F;51-304/Domain: protein kinase homology <KIN>F;59-67/Region: protein kinase ATP-binding motif
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                   (EC 2.7.1.-) kem
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                 kinase
                   protein
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Best Local Similarity 32.6
Matches 199; Conservative
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QY         297 TLEDVASHWWVNWQYTTGVGEQEALREGGHPSGDFGRASMADW 339           11 SLDNIMKDRWMNVGYEDDELKPFIEPPKDQIDEQRIEKLIQIFQLGFNKAAILES 465           QY         340 LRRSSRPLLENGAKVCSFFKQHVPGGGSTVPGLERQHSLKKSRKENDWAQNLQGDPAEDT 399           QY         1   1   1   1   1   1   1   1   1   1	Db 360KFEDIHATYLLLGERKSDMDASEITWAQSLLSHSSINVSSSLGQH- 404  Qy 408 LKLPKGILKKKSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRES 464
Db 564 OKHOGSSARSSGSSSRRSSQNDA-ATA-GCTVVMSGTRHCGVOWRAQPTSRQATISL 622  QY 512 NGKPSRTALEGTTPOTFGSLDQLASSHPAARPS 544  Db 623 LQPPSYKPSSNTTQIAQIPPLFNRNSTATSSAAQPS 658  RESULT 6	RESULT 7 113741 hypothetical protein 22B5.8 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C;Accession: T137H, C;Marchy, L.; Harris, D.; Barrell, B. R;Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data library, April 1999
n H39E23.1 [imported] - Caenorhabditis elegans les: Caenorhabditis elegans : 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 ssion: G89287 ymous, The C. e 282, 2012-2018, 1998 e: Genome sequence of the nematode C. elegans: a platform for investigating biolog rence number: A75000; MUID:99069613; PMID:9851916 rence number: A75000; MUID:99069613; PMID:9851916 rence websites genome.wustl.edu/qsc/C elegans www.sanger.ac.uk/Projects/C_ele	A, Description: Sequencing the distal A Chromosome of Diosophina meranoguect. A, Reference number: 217668 A, Reference number: 217668 A, Accession: T13741 A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Residues: 1-1398 <amr> A, Cross-references: UNIPROT:077268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA21, A, Cross-references: FlyBase:FBGn0000667 A, Cross-references: FlyBase:FBGn0000667 A, Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3</amr>
rata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and 'Y' 'STO> GB:Chr_V, PIDN:CAB09532.1; PID:g3878100; GSPDB:GN00023; CESP:H39E23.	A;Note: EG:22E5.8  Query Match Query Match Best Local Similarity 31.1%; Pred. No. 1.5e-19; Indels 158; Gaps 25; Matches 210; Conservative 92; Mismatches 216; Indels 158; Gaps 25;  Qy 10 PSQAPPSASALASESANPLADGLIKSPKPLMKGNKRHHKGNLRHRYEFLETLGKGTVG 69 1
20.3%; Score 667; DB 2; Length 1246; milarity 31.9%; Pred. No. 1e-19; Conservative 93; Mismatches 199; Indels 96; G KQAVKRHHKGNLRH	Oy 70 KVKKARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFENSK 128
10 67 70	
Qy 126 SSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDLKLENI 185  129 EQTLYLVLEYASGGEVFDYLVAHGRMKEKBARAKFRQIVSAVQYLHSKNIIHRDLKAENL 188  Qy 186 LLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGFBVDSWSLGVLX 245	QY 249 HGTMPFDGQDHKTLVKQISNGAYREPPKPSDAC-GLIRWLLMYNPTRRATLEDVASHWW-306
2 2 2 2 2 3 3 3 3 3 3 5 5 5 5 5 5 5 5 5	QY 341GG 366  Db 448 VAAIYLLLQDRVSHKKEQSNGLGASALASSTSASRMIYSSRNDHOPTQQOSQOOSKTIST 507  QY 367 STVPGLERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLP-KGILKK 417
	Db 508 SSILAKDQCHKRLSRHQTVLMSERNAHAGATPTVPDPGPGYYÄKYGPLQLPLPLTGHSHL 567  Qy 418 KSSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSS 469

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serine/threonine-specific protein kinase (BC 2.7.1.-) AK21 - Arabidopsis thaliana serine/threonine-specific protein kinase SNF1 homolog ($) Species: Arabidopsis thaliana (mouse-ear cress) ($) Species: Arabidopsis thaliana (mouse-ear cress) ($) Species: Arabidopsis thaliana (mouse-ear cress) ($) Species: Arabidopsis thaliana (mouse-ear cress) ($) Accession: JC1446; S58266; S66334 ($) Seed 120, 249-254, 1992 ($) Seed 120, 249-254, 1992 ($) Seed 120, 249-254, 1992 ($) Species: A. Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M. Gene 120, 249-254, 1992 ($) A; Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein A; Reference number: JC1446; MUID:93013041; PMID:1339373 ($) Ascession: JC1446 ($) A; Molecule type: DNA A; Residues: 1-512 clEG ($) A; Cross-references: UMIPROT:038997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g166600 A; Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. Sthuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. Submitted to the BMBL Data Library, May 1995 A; Description: Differential accumulation of the transcripts of 22 novel protein kinase gf A; Reference number: S58256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or peptidyl-threonine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               526 GQVMTGSPATARMTSAFLASQSDAPVLQVQGCMGGASLLPVSFQEGRRASDTSLTQGLKA 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-504 <GUM>
A; Residues: 1-504 <GUM>
A; Cross-references: UNIPROT: P93113; EMBL: Y10036
A; Experimental source: cv. Masterpiece; cotyledon
C; Function:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidy
C; Superfamily: AMP-activated protein kinase; protein kinase homology
C; Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F; 6-260/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                              probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber N.Alternate names: SNF1-related protein kinase (.Species: Cucumis sativus (cucumber) c.bate: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 R;Gumpel, N.J.
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                                                                                                                                                                                                                                                                                                                                    R,Gumpel, N.J.

R,Gumpel, N.J.

Rubmitted to the EMBL Data Library, December 1996

R,Reference number: 217020

A,Accession: T10449

A,Status: preliminary; translated from GB/EMBL/DDBJ
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Matches 127; Conservative
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RITIPEIROHPW 259
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                                                                                              586 FRQQ 589
                                                    598 WWQE 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 VIVMEYASRGDLYDYISERPRISERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVH 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 GSTVPGLERQHSLKK-----SRKENDMAQNLQGDPAEDTSSRPGKSSL
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19.7%; Score 648; DB 2; Length 798;
Best Local Similarity 29.4%; Pred. No. 3.8e-19;
Matches 195; Conservative 94; Mismatches 223; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9IA88; GB:AF219232
C;Comment: This protein, a member of the AMPK/SNF1 family of
C;Gentics:
A;Gene: qik
C;Keywords: protein kinase
                                  499
                                                                                 KSHQKS 427
                                  KSPOAS
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Length 511;

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A;Status: preininary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mSNA
A;Molecule type: mSNA
A;Molecule type: mSNA
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A;Molecule type: mSNA
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C;Molecule type: mSNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPS-DACGLIRWLLMVNPTR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEV
A;Reference number: A56009; MUID:94217693; PMID:8164654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.2%; Score 631; DB 1;
49.6%; Pred. No. 1.2e-18;
tive 48; Mismatches 77;
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Matches 125; Conservative
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A;Status: preliminary
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 144-198 < TH2>
A; Cross-references: EMBL:X86966; NID:9928909; PIDN:CAA60529.1; PID:9928910
C; Comment: This enzyme plays an important role in a signal transduction cascade regulatic cidentics:
A; Comment: This enzyme plays an important role in a signal transduction cascade regulatic cidentics:
A; Comment: This enzyme plays an important role in a signal transduction cascade regulatic cidentics:
A; Comment: This enzyme plays an important role in a signal transduction cascade regulatic cidentics:
A; Comment: This enzyme plays an important role in a signal transduction:
A; Churtcion:
A; Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin c; Superfamily: AMP-activated protein kinase; protein kinase homology
C; Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
C; Superfamily: AMP-activated protein kinase homology
C; Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F; T1-271/Domain: protein kinase homology
C; Keywords: ATA, A44/Active site: Lys, Glu, Asp, Lys #status predicted
F; 147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                 genes
                              A Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
R; Thuemmler, F:; Kirchner, M.; Teuber, R.; Dittrich, P.
R; Thuemmler, F:; Kirchner, M.; Teuber, R.; Dittrich, P.
A; Title: Differential accumulation of the transcripts of 22 novel protein kinase
A; Reference number: S66314; MUID:96123233; PMID:8534852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 GILKKKSSTSSG-----EVQEDPQELRPVPDTPGQPVP--AVSLLPRKGILKKS---- 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.4%; Score 639.5; DB 1;
35.8%; Pred. No. 5.5e-19;
tive 72; Mismatches 139;
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156; Conservative
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Matches 15
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C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
A;Note: in vivo substrates include hydroxymethylglutaryl-CoA reductase (NADPH) and acety
                                                                                                                                                                                                                                                                                                                                                             A; Title: Molecular cloning, expression and chromosomal localisation of human AMP-activat A; Reference number: S51025; MUID:95080410; PMID:7988703
                                      N'Alternate names: AMPK
N'Alternate names: AMPK
N'Contains: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl-CoA C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C; Accession: S51025; ISB503
R; Berls, R.K.; Marley, A.E.; See, C.G.; Sopwith, W.F.; Aguan, K.; Carling, D.; Scott, J. PEBS intt. 356, 117-121, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human homologue of
hydroxymethylglutaryl-CoA reductase (NADPH2)} kinase (EC 2.7.1.109) - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
Amolecule type: mENA
A;Residues: 1-179, '1.181-270,'G', 272-402,'RQ', 405-552 <RES>
A;Ccossereferences: EMBL:U06454; NID:9758366; PIDN:AAA64745.1; PID:9758367
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A;Resdudes: 1-522 <BRRA
A;Cross-references: UNIPROT:P54646
R;Aguan, K.; Scott, J.; See, C.G.; Sarkar, N.H.
Gene 149, 345-350, 1994
A;Title: Characterization and chromosomal localization o
A;Reference number: 138503; MUID:95047501; PMID:7959015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: GDB:PRKAA2; PRKAA, AMPK; hAMPK
A,Cross-references: GDB:451905; OMIM:600497
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A56009

serine/Lhreonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco. Progression Nicotiana tabacum (common tobacco)
CjSpecies: Nicotiana tabacum (common tobacco)
CjSpecies: 28-Apr-1995 #sequence\_revision 28-Apr-1995 #text\_change 09-Jul-2004
CjAccession: A56009
R; Muranaka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces tase of Saccharomyces

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F;33-286/Domain: protein kinase homology <KIN>
                                             Query Match
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                C;Keywords: ATP; magnesium; phosphotransferaes; serine/threonine-specific protein kinase F:14-268/Domain: protein kinase homology «KIN»
F:22-30/Region: protein kinase homology «KIN»
F:23-30/Region: protein kinase ATP-binding motif F:45.64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted
F:144,148/Binding site: magnesium (Asn, Asp) #status predicted
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FOG2 protein - yeast (Kluyveromyces marxianus var. lactis)
FOG2 protein - yeast (Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Species 19-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S72513
R;Goffrini, P.; Fidarelli, A.; Donnini, C.; Lodi, T.; Puglisi, P.P.; Ferrero, I.
Curr. Genet. 29, 316-326, 1996
A;Title: FOG1 and FOG2 genes, required for the transcriptional activation of glucose-rep
A;Reference number: S72513; MUID:96171814; PMID:8598052
A;Accession: S72513
A;Accession: S72513
A;Molecule type: DNA
A;Residues: l-602 cGGF>
A;Cross-references: UNIPROT:P87209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the source is designated as Kluyveromyces lactis
C;Genetics:
A;Gene: FOG2
C;Function:
A;Description: probably involved in the regulation of glucose-repressible gene expressic
C;Superfamily: AMP-activated protein kinase; protein kinase homology
                                                                                                                                                                                     17;
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                                                                                                                                                                                                                      45 KRHHHKHNLRHRYEFLETLGKGTYGKVK-KARESSGRLVAIKSIRKDKIKDEQDLLHIRR 103
                                                                                                                                                                                                                                                                                                         163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 IVNGKPYVGPEVDSWSLGVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPS-DACG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQHVPGGGSTV---- 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---PGL----ERQHSL----KKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSTSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRK-----GILKKSRQR---ESGYYSS 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 ESEVMNSLYSGDPQ----DQLAVAYHLIIDNRRIMNQASE---FYLASSPPSGSFMDDSAM 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358 HIPPGLKPHPERMPPLIADSPKARCPLDAL-----NTTKPKSLAVKKAKWHLGIR 407
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                                                                                                                                                                                                                                                   LIRWLLMVNPTRRATLEDVASHWWVNW-------GYTTGVGEOEALRE-----
                                                                                                                                                                                                                                                                                                     EIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQI
                                                                                                                                                                                     Gaps
Superfamily: AMP-activated protein kinase; protein kinase homology
                                                                                                                                                                                     93;
                                                                                                                                             DB 1; Length 552;
                                                                                                                                         Query Match

19.1%; Score 630.5; DB 1; Length 5
Best Local Similarity 31.5%; Pred. No. 1.3e-18;
Matches 176; Conservative 91; Mismatches 199; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           291 PDYLVPAESTHQENS-----ESKTEDGGPSVPLELIDDSLVQTLSNTMGYDVDEIYEA 343
                                                                                                                                                                                 99 L-HIRREIEIMSSLNHPHIIAIHEVFENSSKIVIVMEYASRGDLYDYISERPRLSERDAR 157
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                                                                                                                      47 HHHKHNLRH-----RYEFLETLGKGTYGKVKKARE-SSGRLVAIKSIRKDKIKDEQDL
                                                                                                                                                                                                                                                                        HFFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSP
                                               Gaps
                                               87;
  Length 602;
                                               Indels
  DB 2;
                                            68; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.1%; Score 627.5; DB ; larity 35.6%; Pred. No. 1.9e-18 Conservative 68; Mismatches 12?
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he : 42.5452 secs
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                     Best Local Similarity
Matches 155; Conserv
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OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

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                                                           Sequence 103, App
Sequence 20, Appl
Sequence 50, Appl
Sequence 101, App
Sequence 102, App
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Sequence 4, Appli
Sequence 274878,
Sequence 70100, A
Sequence 3, Appli
Sequence 22, Appli
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100.0%; Score 3293; DB 14; Length 631;
Best Local Similarity 100.0%; Pred. No. 1.4e-206;
Matches 631; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11, Application US/10355975
Publication No. US20030162277A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Inmunex Corporation
APPLICANT: Wirca, G. Duke
APPLICANT: Wartin, Unja
APPLICANT: Anderson, Dirk M.
ITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-4
CURRENT APPLICATION NUMBER: US/10/355,975
CURRENT FILING DATE: 2003-01-30
PRIOR APPLICATION NUMBER: US/09/579,664B
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
4 US-10-354-358-82

10S-10-723-866-2553

(US-10-318-61-103

(US-10-343-514-103

(US-10-343-514-102

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US-10-425-114-70100
US-09-919-585-3
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US-10-355-975-11
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Sequence 2, Appli
Sequence 640, Appl
Sequence 77, Appl
Sequence 12, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 2, Appli
Sequence 604, Appl
Sequence 6, Appli
Sequence 6, Appli
                                                                                                                                                                                        ; Search time 146.329 Seconds (without alignments) 1557.950 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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US-10-370-715B-640
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US-10-311-034-12
US-10-312-261-26
US-10-363-829-504
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US-10-322-281-23
US-10-343-514-41
US-09-963-159-2
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US-09-780-949-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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APPLICANT: BRUCKER, Daniel J.
APPLICANT: ROSEN, Cheryl F.
APPLICANT: ROSEN, Cheryl F.
TITLE OF INTENTION: AMPR.RELATED SERINE/THREONINE KINASE, DESIGNATED SNARK
FILE REFERRING: DPA-DRUCZ/PCT
CURRENT APPLICATION NUMBER: US/10/343,514
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: PCT/CA01/01109
PRIOR FILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PELING DATE: 2001-08-12
PRIOR APPLICATION NUMBER: US 60/224,613
PRIOR PELING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: CA 2,340,780
PRIOR PILING DATE: 2001-03-28
NUMBER OF SEC ID NOS: 109
SOFTWARE: PATENTING DATE: 2001-03-28
NUMBER OF SEC ID NOS: 109
SOFTWARE: PATENTING DATE: 2001-03-28
NUMBER OF SEC ID NOS: 109
SEC ID NO 41
LENGTH: 630
                    249
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                                                        GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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Best Local Similarity
Matches 593; Conserva
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US-10-343-514-41
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                                                                                          HVPGGGSTVPGLERQHSLKKSRKENDWAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKSS
                          EVFENSSKIVIVMEYASRGDLYDYISERPRLSERDARHFFRQIVSALHYCHQNGIVHRDL
                                                                      KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
                                                                                                                                                  GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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US-10-322-281-23

10-322-281-23

1 Sequence 23, Application US/1032281

1 Fublication No. US20040126762A1

1 GENERAL INFORMATION:
1 APPLICANT: David W. Morris
1 APPLICANT: Marc S. Malandro
1 TILE OF INVENTION: Novel Compositions and Methods in Cancer
1 FILE REFERENCE: 529452001000

1 CURRENT APPLICATION UNDRER: US/10/322,281

2 CURRENT FILING DATE: 2002-12-17

3 NUMBER OF SEQ ID NOS: 866

3 SOFTWARE: FastSEQ for Windows Version 4.0

3 SEQ ID NO 23
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98.3%; Pred. No. 1.4e-199;
tive 0; Mismatches 1;
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ORGANISM: Mus musculus
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Matches 620;
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US-10-322-281-23
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Sequence 4A Application US/10423543

Publication No. US20040058355A1

SEQUENCE 4A Application DEPLANCE

Publication No. US20040058355A1

SEQUENCE AL INFORMATION:

APPLICANT: Milbermann, Roaman K.

APPLICANT: Milbermann, Roaman K.

APPLICANT: Milbermann, Roaman K.

APPLICANT: Midolph-Owen, Laura A.

APPLICANT: Curtis, Rory A.J.

APPLICANT: Teal, Foog-Ying

APPLICANT: Teal, Foog-Ying

APPLICANT: Teal, Foog-Ying

APPLICANT: Teal, Foog-Ying

APPLICANT: Bandaru, Rajaeckha 5634, 55053, 2504, 15977,

ITILE OF INVENTION: 14760, 25504, 17903, 3700, 21529, 26176, 26348, 56638

ITILE OF INVENTION: 14760, 25504, 17903, 3700, 21529, 26176, 26348, 56638

ITILE OF INVENTION: 14760, 25504, 17903, 3700, 21529, 26176, 26348, 26078

ITILE OF INVENTION: 14760, 25504, 17903, 39056

FILE REFERENCE: WRIO3-0230MIN, 14760, 2564, 256447

FILE REFERENCE: WRIO3-0230MIN, 14760, 256447

FRIOR APPLICATION NUMBER: US 50/214, 216

PRIOR PLILING DATE: 2000-11-03

CURRENT FILING DATE: 2000-11-03

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR PLILAGION NUMBER: US 50/248, 325

PRIOR PLILAGION NUMBER: US 60/248, 325

PRIOR PLILAGION NUMBER: US 60/248, 893

PRIOR PRIOR APPLICATION NUMBER: US 60/248, 893

PRIOR PRING DATE: 2000-11-15

PRIOR PRING DATE: 2000-11-15

PRIOR PRING DATE: 2000-11-15

PRIOR PRING DATE: 2000-11-15

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PRIOR PRING DATE: 2000-11-15

PRIOR PRING DATE: 2000-11-15
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                                                                             GVLLYILVHGTMPFDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLED
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                                                                                                     TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
                              KLENI LLDANGNI KIADFGLSNLYHQGKFLQTFCGSPLYASPEI VNGKPYTGPEVDSWSL
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        KLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSL
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VASHWWVNWGYTTGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQ 360
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Patent No. US20020077312A1
GENERAL INFORMATION:
APPLICANT: Cuttis, Rory A.J.
APPLICANT: Calvin, Katherine M.
TITLE OF INVENTION: 3700, A NOVEL HUMAN PROTEIN KINASE AND USES THEREFOR FILE REFRENCE: 10.47-500.
CURRENT APPLICATION NUMBER: US/09/963,159
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
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85.8%; Score 2824.5; DB 9;
Best Local Similarity 85.7%; Pred. No. 5.4e-176;
Matches 544; Conservative 26; Mismatches 54; I
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; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                       85.8%; Score 2824.5; DB 15; Length
85.7%; Pred. No. 5.4e-176;
ive 26; Mismatches 54; Indels
                                                                           Wrapper
                                                                         File 1
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                                                                         See
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 60/186,061
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 10/217,168
PRIOR FILING DATE: 2002-08-12
Remaining Prior Application data removed - S.
NUMBER OF SEQ ID NOS: 119
SEQ ID NO 44
                                                                                                                                                                                                    Query Match
Best Local Similarity 85.7°
Matches 544; Conservative
                                                                                                                                                            ORGANISM: Homo Sapiens
                                                                                                                                                                          US-10-423-543-44
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3

Sequence 640, Application US/10370715B
Publication No. US20040258678A1
GENERAL INFORMATION:
Patin Docket Preview
APPLICANT: BODAX, SARAH C.
APPLICANT: CLARK, HILLARY
APPLICANT: BAISDELL, HUNTE
APPLICANT: JACKMAN, JANET

RESULT 6 US-10-370-715B-640

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|||| MESLVFARRSGPTPS----AAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFL
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                                                                         Methods for the Treatment of
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               APPLICANT: WILLIAMS, P. MICKEY
APPLICANT: WOOD, WILLIAM I.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Related Diseases
FILE REFERENCE: P1948R1-US
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
SEQ ID NO 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 77, Application US/10618941; Publication No. US20040197792A1; GENERAL INFORMATION:
SCHOENFELD, JILL R. WILLIAMS, P. MICKEY WOOD, WILLIAM I. WU, THOMAS D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WHYTE, DAVID
APPLICANT: MANNING, GERARD
APPLICANT: CAENEPEEL, SEAN
                                                                                                                                                                                                                                                                                                           Best Local Similarity 85.73
Matches 544; Conservative
                                                                                                                                                                                                                                     ORGANISM: Homo sapien
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Best Local
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APPLICANT: KHAH, Farrah A.
APPLICANT: KHAH, Farrah A.
APPLICANT: KECTPON, Shirley A.
APPLICANT: RECIPON, Shirley A.
APPLICANT: AZIMZAI, Yalda
APPLICANT: POLICKY, Jennifer L.
APPLICANT: DING, Li
APPLICANT: GRETHER, Megan
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: THANGAVELU, Kavitha
APPLICANT: BATRA, Sajev
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/212,073; 60/215,651; 60/216,605; 60/218,372; 60/228,066
PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-07-07; 2000-07-13; 2000-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 FFRQIVSALHYCHQNGIVHRDLKLENILLDANGNIKIADFGLSNLYHKGKFLQTFCGSPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.6%; Score 2720.5; DB 15; Length 594; Best Local Similarity 87.3%; Pred. No. 3.1e-169; Matches 521; Conservative 22; Mismatches 47; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
TOTHER INFORMATION: Incyte ID No. US20040023242A1 4841542CD1
US-10-311-034-12
                                                          Σ
                                     GANDHI, Ameena R.
TRIBOULEY, Catherine
CHAWLA, Narinder K.
                                                                                                                                                                                                                                                                                                           HAFALIA, April
ARVIZU, Chandra S.
GURURAJAN, Rajagopal
                                                                                                                                               RAMKUMAR, Jayalaxmi
GRIFFIN, Jennifer A.
KEARNEY, Liam
                                                                                                                                                                                                                    NGUYEN, Danniel B.
TANG, Y. Tom
BAUGHN, Mariah R.
                                                                                          YAO, Monique G.
LU, Dyung Aina M.
GREENWALD, Sara R.
                                                                                                                                                                                                                                                                           HE, Ann
THORNTON, Michael
                                                                                                                                                                                                                                                                                                                                                                   LO, Terence P
KHAH, Farrah A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 12
LENGTH: 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
               GANDHI
                                                                                                                                                                                                     BURFORD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279
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APPLICANT:
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                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                      1 85.8%; Score 2824.5; DB 17; Length 672; Similarity 85.7%; Pred. No. 5.9e-176; Hy, Conservative 26; Mismatches 54; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 RWWQESLGDSCFSLTDCQEVTAAYRQALGICSKLS 631
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CURRENT APPLICATION NUMBER: US/10/618,941
PRIOR APPLICATION NUMBER: 60/395,632
PRIOR FILING DATE: 2002-07-15
NUMBER OF SEQ ID NOS: 143
SEQ ID NO 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 12, Application US/10311034
; Publication No. US20040023242A1
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: LAL, Preeti
; APPLICANT: BANDMAN, Olga
; APPLICANT: BOROWSKY, Mark L.
TITLE OF INVENTION: NOVEL KINASES
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.73
Matches 544; Conservative
                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                     ; ORGANISM: HOI
US-10-618-941-77
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481 ASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTALEGTTPSTFGSLDQLASSHPA 540
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                                      TSSGEVQEDPQELRPVPDTPGQPVPAVSLLPRKGILKKSRQRESGYYSSPEPSESGELLD
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Sequence 404, Application US/10363829

Publication No. US20040142331A1

Sequence 404, Application US/10363829

Publication No. US20040142331A1

SEGNERAL INFORMATION:

APPLICANT: Jackson, Struatt E., Lincoln, Stephen E.;

APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;

APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;

APPLICANT: Gradley, Michael S.; Jackson, Jennifer L.;

APPLICANT: Hardis, Rachel J.; Gateren, Darryl;

APPLICANT: Bradley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Bradley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Brandley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Brandley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Gradley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Gradley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Gradley, Diana L.; Rohatgi, Samer D.;

APPLICANT: Marwha, Rakesh, Chen, Alice J.;

APPLICANT: Marwha, Rakesh, R.

APPLICANT: Marwha, Rakesh, R.

APPLICANT: Marwha, Rakesh, R.

TITLE OF INVENTION NUMBER: US/003-05

CURRENT FILING DATE: 2000-03-05

PRIOR FILING DATE: 2000-09-05

PRIOR FILING DATE: 2000-09-05

PRIOR FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: US 60/229,749

PRIOR FILING DATE: 2000-09-05

PRIOR FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: US 60/229,749

PRIOR APPLICATION NUMBER: US 60/229,749

PRIOR FILING DATE: 2000-09-05

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PRIOR PLING DATE: 2000-0
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SOFTWARE: PERL Program
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NAME/KEX: misc feature

OTHER INFORMATION: Incyte ID No: LG:982800.1.orf1:2000SEP08
US-10-363-829-404
                                                                                                                                                                                                                                                                                                                                                                                                              584 RWRQDPLGDSCFSLTDCQEVTA--YQALRVCSKLT 616
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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/230,597
PRIOR FILING DATE: 2000-09-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo
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                                                             459 SRQRESGYYSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRT 518
                                                                                                                                                                                                                                                                                                                   418 PRQRESGYYSSPEPSESGGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQT 477
                                                                                                                                                                                                                                                                                                                                                                                                    519 ALEGTIPSTFGSLDQLASSHPAARPSRPSGAVSEDSILSSESFDQLDLPERLPETPLRGC 578
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ETLGKGTYGKVKKARESSGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/10322281

Publication No. US20040126762A1

GENERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: David W. Morris

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REPERENCE: 529452010100

CURRENT APPLICATION WUMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 616
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82.4%; Score 2712.5; DB 16; Length
Best Local Similarity 84.3%; Pred. No. 1.1e-168;
Matches 535; Conservative 25; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-281-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 YSSPEPSESGELLDAGDVFVSGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPT
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                                                                                                                                       - See File Wrapper or PALM
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Sequence 2, Application US/09780949;
Patent No. US20020006618A1
GAPERRAL INFORMATION:
APPLICANT: Kapeller-Liberman, Rosana
TITLE OF INVENTION: Methods for Using 20893, a Human Protein
TITLE OF INVENTION: Methods for Using 20893, a Human Protein
TITLE OF INVENTION: Kinase
FILE REFERENCE: 035800/209015
CURRENT FILING DATE: 2001-02-09
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,690
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 6
SO ID NO 2
LENGTH 661
LENGTH 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 406;
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                                                                                                                                                                                                                                                                                                                                                     FRATURE:
NAMB/KEX: misc_feature
CTHER INFORMATION: Incyte ID No: LI:1144409.1.orf1:2000SEP08
US-10-363-829-504
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PRIOR APPLICATION NUMBER: US bu/220,220
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: US 60/230,597
PRIOR FILING DATE: 2000-09-06
Remaining Prior Application data removed - 8
NUMBER OF SEQ ID NOS: 506
SOFTWARE: PERL Program
SEQ ID NO 504
SEQ ID NO 504
                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: H. E
US-09-780-949-2
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US-09-780-949-2
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APPLICANT: Chalup, Michael S.; Jackson, Gerard E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Jones, Aniesa L.; Yu, Jimmy Y.;
APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
APPLICANT: Dahl, Christopher R.; Momiyama, Monika G.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Geretin, Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: Geretin, Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: Geretin, Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: Geretin, Jr., Edward H.; Peralta, Careyna H.;
APPLICANT: Marwaha, Rakesh; Chan, Alice J.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
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APPLICANT: Chang, Simon C.; Au, Alan P.;
APPLICANT: Chang, Simon C.; Au, Alan P.;
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APPLICANT: Chang, Simon C.;
APPLICANT: Chang, Simon C.;
APPLICANT: Chang, Simon C.;
APPLICAN
            54.1%; Score 1781.5; DB 16; Length 406; 83.6%; Pred. No. 4.1e-108; ive 16; Mismatches 44; Indels 7;
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                                                                          44; Indels
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                                         Best Local Similarity 83.6
Matches 342; Conservative
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Gaps

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US-09-780-949-6

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ARES-SGRLVAIKSIRKDKIKDEQDLLHIRREIEIMSSLNHPHIIAIHEVFENSSKIVIV 132
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                                                                             13 PDLGLGAPGSPREAVAGATAALEP-RKPHGVKRHHHKHNLKHRYELQETLGKGTYGKVKR
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al Similarity 55.5%; Pred. No. 1.7e-102; 372; Conservative 74; Mismatches 151;
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Patent No. US20020006618A1;
GENERAL INFORMATION:
APPLICANT: Kapeller-Liberman, Rosana.
APPLICANT: Waich, Nadine S.
APPLICANT: Galvin, Katherine M.
ITILE OF INVENTION: Methods for Using 20893, a F.
ITILE OF INVENTION: Methods for Using 20893; a F.
ITILE OF INVENTION: Minase
FILE REFERENCE: 035800/209015
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,690
PRIOR FILING DATE: 2000-02-09
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SOFTWARE: FABLSEQ for
SEQ ID NO 6
LENGTH: 661
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ORGANISM: H. sapiens
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                                                  14 PSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKK
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                    73;
 661;
 Length
                     Indels
 DB 9;
                    74; Mismatches 151;
           1.7e-102;
51.6%; Score 1699.5; 55.5%; Pred. No. 1.7e
         Similarity 55.5% 12; Conservative
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          Best Local Simi
Matches 372;
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APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma Modulators
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05892.0193.NPUS01
CURRENT PEPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR PILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
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      479 YSSPERSESELLDSNDVM--GSSIPSPSPPDPARVTSHSLSCRRKGILKHSSKYSAGTM
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                                               EGTTPS----TFGSLDQ-----LASSHPAARPSRPSGAVSEDSILSSESFDQLDLPER
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 2553, Application US/10723860 Publication No. US20040253606A1 GENERAL INFORMATION:
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US-10-723-860-2553
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Best Local Similarity
Matches 372; Conserv
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TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943, TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099, TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES FILE REFERENCE: MPIO2-020PIRNOMIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGVGEQEALREGGHPSGDFGRASMADWLRRSSRPLLENGAKVCSFFKQHVPGGGSTVPGL 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEYASRGDLYDYISERPRISERDARHFFRQIVSALHYCHQNGIVHRDLKLENILLDANGN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IKIADFGLSNLYHKGKFLQTFCGSPLYASPEIVNGKPYVGPEVDSWSLGVLLYILVHGTM 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEDGQDHKTLVKQISNGAYREPPKPSDACGLIRWLLMVNPTRRATLEDVASHWWVNWGYT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSVCDCDALHDSESPL----LARIIDWHHRSTGLQADTEAKWKGLAK---PTTSEVM--L 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERQHSLKKSRKENDMAQNLQGDPAEDTSSRPGKSSLKLPKGILKKKS----STSSGEVQ 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------EDPQEL----RPVPDTPGQPVPAVS-LLPRKGILKKSRQRESGY 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 PSASALASESARPLADGLIKSPKPLMKKQAVKRHHHKHNLRHRYEFLETLGKGTYGKVKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.6%; Score 1699.5; DB 14; Length 661; 55.5%; Pred. No. 1.7e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74; Mismatches 151; Indels
                                                                            CURRENT PEPLICATION NUMBER: US/10/354,358

CURRENT PELLING DATE: 2003-01-30

PRIOR PELLING DATE: 2003-01-30

PRIOR PELLING DATE: 2003-01-30

PRIOR PELLING DATE: 2002-01-31

PRIOR PELLING DATE: 2002-03-15

PRIOR PELLING DATE: 2002-04-09

PRIOR PELLING DATE: 2002-04-09

PRIOR PELLING DATE: 2002-04-10

PRIOR PELLOATION NUMBER: US 60/371,507

PRIOR PELLOATION NUMBER: US 60/371,507

PRIOR PELLOATION NUMBER: US 60/372,984

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-04-19

PRIOR PELLING DATE: 2002-05-24

PRIOR PELLING DATE: 2002-05-31

PRIOR PELLING DATE: 2002-05-31

PRIOR PELLING DATE: 2002-06-13

PRIOR PELLING DATE: 2002-06-13

PRIOR PELLING DATE: 2002-06-13

PRIOR PELLING DATE: 2002-06-17

PRIOR PELLING DATE: 2002-06-17

PRIOR PELLING DATE: 2002-06-17
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467 YSSPEPSESGELLDASDVFVSGDPVEQKSPQASGLLLHRKGILKLNGKFSRTAL 520	521 EGTTPSTPGSLDQLASSHPAARPSRPSGAVSEDSILSSESFDQLDLPER 569 :	570 LP-ETPLRGCVSVDNLRGLEQPPSEGLKRWWQESLGDSCFS-LIDCQEVTAAYR 621	622 QALGICSKLS 631                 61 652 QALEICSKLN 661
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Search completed: January 22, 2005, 07:00:33 Job time : 150.329 secs